Genetic evaluation of functional longevity in South African Holstein cattle using a proportional hazards model

by

Venancio Edward Imbayarwo-Chikosi

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Supervisor: Prof. K. Dzama
Co-supervisor: Dr. C.B. Banga
Co-supervisor: Dr. T.E. Halimani

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Declaration

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ABSTRACT

Improvement and selection of superior animals for longevity is a viable complimentary strategy for increasing functional longevity of Holstein dairy cattle. Genetic evaluation of animals for functional longevity is a prerequisite for improvement of the trait. This study was carried out to determine non-genetic factors that influence functional longevity in South African Holstein cattle, as well as to estimate genetic parameters for functional longevity, estimate sire breeding values, and to establish the contribution of conformation traits to the risk of cows being culled from dairy herds. Analyses were carried out using records of 166 222 daughters of 2 051 sires from 1 545 herds in six regions of South Africa. The regions were the Western Cape, Eastern Cape, Northern Cape, Free State, Kwa-Zulu Natal and the combined Gauteng & North Western Provinces. Data were analysed using a piecewise Weibull sire-maternal grandsire model in which the baseline hazard was assumed to change at 270 and 380 days in milk as well as at drying-off. The fixed effects model comprised of the time-independent effect of age at first calving, the combined time-dependent effects of region x year of calving, number of lactations x within-herd milk production class, year of calving x within-herd protein and year of calving x fat percentage production class. Model also had the combined time-dependent effect of herd size x annual herd size change. The random herd-year and sire effects were later included in the model for the estimation of sire and herd-year variance components. Analyses indicated a decline in the survival function, an indicator of functional longevity, among cows that calved for the first time in 2000, 2004 and 2008. Cows that delivered their first calf in 2000 had better survival functions that those that calved for the first time in 2004 and 2008. All fitted effects significantly contributed to the risk of a cow being culled from a herd. Within-herd milk production made the largest contribution to the risk of a cow being culled from a herd. Survival was best in the Northern Cape and worst in Eastern Cape. The risk of being culled was the highest for cows in the second stage of lactation (271- 380 days), when the entire lactation period was considered. High producing cows were more likely not to be culled from a herd than poor producing cows. Cows were more likely to be culled for low protein production percentage than within-herd fat production percentage. The risk of being culled was low for heifers calving at 20 to 25 months of age. The higher risk of culling among cows with multiple lactations indicated the culling policy of dairy farmers to retain a higher number of younger cows than older cows in herds. A decrease in herd size was indicative of a high culling rate. Effective heritability was 0.109. Breeding values ranged from 2.12 for the best cows to -4.80 for the worst cows. This implied that the best and the worst cows were 2.12 times and 4.80 more likely to be culled from herds than the average cow respectively. Genetic trends for functional longevity indicated a marginal decline in sire estimated breeding values. This corresponded with the phenotypic decline in the survivor function observed in cows that calved in 200, 2004 and 2008. All udder, rump, body, feet and leg type traits, with the exception of rear leg side, significantly influenced functional longevity. Farmers culled cows mainly of extremely poor type with a tendency to retain animals with poor to very good structure. Udder traits contributed the most

to the risk of a cow being culled. Cows were more likely to be culled for poor scores received for rear teat placement, rear udder height and fore udder attachment, than for any of the other conformation type traits. The contribution of angularity to the risk of being culled was also high, indicating a preference for highly angular bodied cows. Conformation type traits can therefore be used as indicator traits for functional longevity in Holstein cattle, especially when selection and culling is done based on very poor scores for udder traits. The study indicated that genetic improvement in functional longevity can be achieved with the evaluation and selection of dairy sires. There is therefore a wide scope for including functional longevity in the selection objectives for South African Holstein cattle. There is a need to develop appropriate models to ensure that the national dairy industry can benefit from using a Weibull piecewise model.

Keywords: Holstein cattle, functional longevity, proportional hazards model, Weibull

OPSOMMING

Die verbetering en seleksie van voortreflike diere vir langlewendheid is 'n lewensvatbare en aanvullende strategie vir die verhoging van die funksionele langlewendheid van Holstein melkbeeste. Die genetiese evaluasie van melkproduserende diere ten opsigte van hierdie eienskap is ’n voorvereiste om verbetering in die eienskap moontlik te maak. Die studie is uitgevoer om nie-genetiese faktore wat die funksionele langlewendheid van Suid-Afrikaanse Holsteins beïnvloed te bepaal, om genetiese parameters vir langlewendheid en vaar teeltwaardes vir dié eienskap te bepaal en ook om die bydrae van bouvorm eienskappe tot die waarskynlikheid van koeie om uitgeskot te word, te bepaal. ’n Databasis bestaande uit rekords van 166 222 dogters van 2 051 vaars, wat in ses streke in Suid-Afrika (Wes-Kaap, Oos-Kaap, Noord-Kaap, Vrystaat, KwaZulu-Natal en die gekombineerde Gauteng en Noord-Wes Provinsies) voorgekom het, is vir die studie gebruik. Data is ontleed met behulp van 'n stuksgewyse Weibull vader-moeder grootvader model, waarin die basislyn risiko aanvaar is om te verander op 270, 380 dae na kalwing en by afdroog van die melkkoeie. Die vaste effek model het die tyd-onafhanklike effek van ouderdom met eerste kalwing en die tyd-afhanklike effekte van streek en jaar van kalwing, aantal laktasies en binne-kudde melkproduksie klas, binne-kudde proteïen en vet persent produksie klasse volgens jaar van kalwing, asook die gekombineerde tyd-afhanklike effek van kuddegrootte en jaarlikse verandering in kudde grootte, ingesluit. Die ewekansige trop-jaar en vaar effekte is later opgeneem in die model vir bepaling van die vaar- en kudde-jaar variansie komponente. Ontledings het aangedui dat daar 'n algemene afname in die oorlewingsfunksie, wat ’n aanduiding van funksionele langlewendheid is, was in koeie wat vir die eerste keer in 2000, 2004 en 2008 gekalf het. Koeie wat vir die eerste keer in 2000 gekalf het, het ’n hoër waarde vir die oorlewingsfunksie gehad as koeie wat onderskeidelik in 2004 en 2008 gekalf het. Alle vaste effekte het betekenisvol tot die waarskynlikheid van ’n koei om uitgeskot te word, bygedra. Binne-kudde melkproduksie het die grootste bydrae tot die waarskynlikheid van ’n koei om uitgeskot te word, gemaak. Wanneer die totale laktasieperiode in ag geneem is, was daar gevind dat koeie wat in die tweede fase van laktasie (271-380 dae) die hoogste risiko ervaar het om uitgeskot te word. Hoë produseerders, wanneer hulle met lae produseerders vergelyk is, was minder geneig om uitgeskot te word. Koeie was meer geneig om uitgeskot te word vir lae proteïen produksie persentasie as binne-kudde vet produksie persentasie. Die waarskynlikheid om uitgeskot te word, was laag vir verse wat op ’n ouderdom van 20 tot 25 maande gekalf het. Die hoër risiko van uitskot van koeie met veelvuldige laktasies het aangedui dat melkboere geneig was om meer jonger koeie te behou en ouer koeie uit te skot. ’n Afname in kuddegrootte was aanduidend van ’n hoë uitskotpersentasie. Die effektiewe oorerflikheid was 0.109, met teelwaardes wat van 2.12 vir die hoogste produserende koeie tot -4.80 vir die laagste produserende koeie, gewissel het. Hierdie waardes het dus aangedui dat hoë produseerders en swak produseerders onderskeidelik ’n 2.12 en 4.80 groter kans gehad het om uitgeskot te kan word.

Genetiese tendense vir funksionele langlewendheid het aangedui dat daar 'n marginale afname in vaar beraamde teelwaardes vir funksionele langlewendheid was. Dit het ooreengestem met die waargenome fenotipiese afname in die oorlewingsfunksie wat in 2000, 2004 en 2008 gekalf het. Alle bou-tipe eienskappe (uier, agterkwart, liggaam, voet en been), met die uitsondering van die agterbeen kant, het funksionele langlewendheid betekenisvol beïnvloed. Boere het koeie hoofsaaklik op uiters swak boutipe uitgeskot, met 'n neiging om diere wat as ’n swak tot uiters goeie bouvorm geklassifiseer is, te behou. Uier eienskappe het die meeste tot die waarskynlikheid van ’n koei om uitgeskot te word, bygedra. Koeie met ’n lae gradering vir agterste speen plasing, agter-uier hoogte en voor-uier aanhegting se waarskynlikheid om uitgeskot te word, was groter. Die bydrae van hoekigheid tot die waarskynlikheid van ’n koei om uitgeskot te word was hoog, wat ’n aanduiding van ’n voorkeur vir 'n baie growwe hoekigheid was. Bouvorm tipe eienskappe kan dus gebruik word as indikator eienskappe vir funksionele langlewendheid in Holstein melkbeeste, veral wanneer in ag geneem word dat die meeste melkboere seleksie op grond van swak gradering van uier eienskappe doen. Die studie het aangedui dat genetiese verbetering in funksionele langlewendheid teweeg gebring kan word met die evaluering en seleksie van Holstein vaars. Daar is dus ’n geleentheid vir die insluiting van funksionele langlewendheid in die seleksie doelwitte vir Suid-Afrikaanse Holstein beeste. Daar is ’n behoefte om toepaslike modelle te ontwikkel wat met die toepassing daarvan, sal verseker dat die plaaslike melkbedryf sal kan voordeel trek deur die gebruik van 'n stuksgewyse Weibull model benadering.

Sleutelwoorde: Holstein melkbeeste, funksionele langlewendheid, proporsionele risiko model, Weibull

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CHAPTER 1: INTRODUCTION

1.1 Background

Functional longevity as a component of herd profitability has increasingly become an important trait in dairy cattle evaluations. The main determinants of functional longevity have been described as voluntary culling (e.g. due to low production) or involuntary culling (e.g. due to health or conformation traits). A decrease in involuntary culling increases opportunities for voluntary culling and retention of high yielding cows in herds for longer periods. This leads to an increase in the proportion of mature cows that produce more milk than young ones (Vukasinovic *et al*., 2001) whilst lowering the proportion of the latter. The former are therefore allowed to approximate their maximum production potential as determined by their age (Strapák *et al*., 2005). The corresponding decline in the proportion of younger cows leads to a reduction in costs associated with the supply of energy and protein to these cows. Young cows require the high quality nutrients for the yet to be attained physiological maturity as well as sustaining lactation and pregnancy. Subsequently, farmers will have better control of production costs associated with rearing and purchase of replacement of heifers as there are more heifers for sale (Banga, 2009).

A number of countries have widened their breeding objectives for various dairy cattle breeds to include longevity analysed with survival analysis models and other functional traits such as fertility and mastitis resistance (Carlén *et al*., 2005; Sewalem *et al*., 2005). These include France, United States of America, Germany and New Zealand. In South Africa, the adoption of the balanced breeding concept led to the development of the Holstein Profit Ranking (HPR) index, which has already been adopted by the South African dairy industry. This HPR index combines sire/animal breeding values and economic values for the five traits that directly influence farm profitability: milk volume, protein, fat, somatic cell count and calving interval, each included with an appropriate economic weighting relating to its overall contribution to profitability. Apparently type traits, longevity, live weight and mastitis resistance are not yet part of this HPR index although their economic values are known (Banga, 2009). The breeding values of animals for these traits are yet to be determined using an appropriate method that can handle data on survival and other traits in an optimal way for the South African Holsteins. The aim of this study was therefore to develop a model for prediction of animal breeding values for functional longevity in South African Holstein cattle, estimate the genetic parameters for longevity and to predict the sire breeding values for the trait. The contribution of type traits to the overall risk of culling among Holsteins in South African Holsteins was also estimated.

1.2 Problem statement

Previous studies have shown a consistent decline in longevity among the Holstein cattle in South Africa. This is despite the fact that functional longevity is one of the most economically important traits in South African dairy herds (Banga *et al*., 2014). The decline could be due to lack of evaluation and selection of animals for longevity and the subsequent exclusion of the trait from HPR index for South African Holsteins. Selection among Holsteins is currently therefore on traits other than longevity, yet the superiority of animals on these traits only increase dairy productivity for as long as the animals can resist voluntary and involuntary culling. High yielding cows with short length of productive lives do not justify the rearing costs expended on them. Recent genetic analysis of longevity in South African Jersey cattle reported low heritability estimates, within the range 0.02 to 0.03 and 0.01 to 0.03, with sire and linear multivariate animal models respectively (du Toit, 2011). These linear mixed models cannot be used for South African Holsteins since they have been criticised as being inappropriate for survival data analysis (Vukasinovic, 1999; van der Westhuizen *et al*., 2001; Caraviello *et al*., 2004a). They cannot appropriately handle censored records and the time-dependence nature of non-genetic factors such as herd size, management, production, lactation number, season and year of calving, all of which have a direct influence on the probability of a cow being culled (du Toit, 2011). Besides, linear models assume that effects of environmental factors on the response variable (survival times) are additive when in actual fact they are multiplicative (Flynn, 2012).

1.3 Justification

The South Africa dairy industry has adopted the HPR index system which defines the overall breeding objective of Holstein animals in Rand (ZAR) terms. This breeding objective is derived from a function combining economic and breeding values for traits of importance. The economic values for production, calving interval, somatic cell count and longevity for South African dairy populations have been estimated (Banga, 2009). Functional longevity is not included in the HPR index although its economic values, ranging from 37% of protein's economic value to 36% more valuable than protein in both Jersey and Holsteins, compare favourably with those for milk volume, butterfat content and calving interval South Africa. Any breeding objective developed for South African Holsteins should therefore include functional longevity. Currently, this is not possible because breeding values of South African Holstein sires for functional longevity have not been estimated. It is therefore necessary, through this study, to estimate breeding values for longevity among Holsteins using methodologies that can handle survival data, consisting of complete (uncensored) and incomplete (censored) records, in an optimal way for subsequent inclusion into the HPR index.

When used as indirect selection criteria for functional longevity, type traits offer several advantages over direct selection on functional longevity (Weigel *et al*., 1998) which makes selection on type traits relatively more attractive. The genetic correlation between udder traits and functional herd life in Holsteins has been reported positive within the range of 0.22 and 0.48 (Setati *et al*., 2004). This would imply that selection for udder traits can be useful in improving functional longevity. However, the extent to which functional longevity is influenced by involuntary culling on the basis of compromised udder type traits in South African herds is not known i.e. the magnitude of the risk of culling due to defective udder type traits is not known. By extension, the effect of specific type traits on actual duration of productive herd life is not known. The linear mixed model methodologies used recently to genetically evaluate longevity and type traits do not offer themselves for determination of risk ratios for the culling risk. The use of proportional hazards models in this study will provide an ideal tool for determining the true phenotypic correlation between longevity and type traits (Ducrocq *et al*., 1988). If this study establish that the type traits contribute largely to culling risk and culling in dairy herds, strategies could be adopted for combining functional longevity and type traits in a selection index to increase efficiency of selection of animals.

1.4 Objectives

The study was carried out to genetically evaluate functional longevity in South African Holstein cattle using proportional hazards models. The specific objectives of the study were: -

1.4.1 To determine the time-dependent and time-independent factors that influence functional longevity in the SA Holstein cattle population;

1.4.2 To determine effective and equivalent heritability estimates for functional longevity in SA Holstein cattle using the proportional hazards models;

1.4.3 To estimate sire breeding values for functional longevity;

1.4.4 To determine the contribution of udder traits, rump, body, feet and leg traits to the relative risk of culling and therefore functional longevity;

1.5 Hypothesis

The following hypotheses were tested: -

1.5.1 Functional longevity in South African Holsteins is not influenced by time-dependent and time-independent non-genetic factors;

1.5.2 The length of productive life is not heritable;

1.5.3 Type traits do not contribute to the risk of culling in South African Holstein catlle.

1.6 Layout of the chapters

This dissertation consists of six chapters; an introduction, literature review, three research chapters and a general conclusions and recommendations chapter. Each of the three research chapters has its own abstract, introduction, materials and methods, results, discussion, conclusion and references.

Chapter 1: General Introduction

This chapter provides general background information outlining the wider gaps to be investigated in the study. The chapter has an introduction, problem statement, justification, objectives and hypotheses. It also presents the general layout of the dissertation.

Chapter 2: Literature Review

This chapter focuses on discussion of various genetic models that have been used previously to evaluate functional longevity in dairy cattle. It highlights some non-genetic factors that have been identified in previous research to influence functional longevity and also explains the relationship between longevity and conformation traits.

Chapter 3: Non-genetic factors influencing functional longevity in South African Holstein cattle

The chapter describes the fixed effects piecewise Weibull proportional hazards model for establishing factors (covariates) that contribute to the risk of culling of dairy cows. The significance of the covariates is determined and their relationship with the relative risk of culling, a direct measure of longevity is demonstrated through plots. These identified fixed covariates will be adjusted for in the mixed model estimation of variance components. A non-parametric cox model that was run to estimate overall longevity across and within lactations is also presented in this chapter.

Chapter 4: Genetic parameters for longevity in the South African Holstein cattle from proportional hazards models

The frailty (mixed) model for estimation of random sire and herd-year variance is presented. Random effects are estimated and both effective and equivalent heritability of functional longevity are estimated. Sire proofs are determined using output from survival analysis. The effective heritability

is used to estimate reliability of the sire proofs. Equivalent heritability is estimated incorporating proportion of uncensored daughters (p) derived from the global cox model.

Chapter 5: The relationship between conformation traits and functional longevity in South African Holstein cattle

The chapter evaluates the contribution of type traits to the risk of cow culling through incorporation of the type traits, one at a time, in the Weibull model developed in earlier chapters. Traits with the greatest impact on the risk of culling and therefore functional longevity are identified and prospects for their use as indicator traits for longevity are presented.

Chapter 6: General conclusions and recommendations

This chapter gives general conclusions of the current study, provides recommendations for the Holstein cattle dairy industry and gives perspectives for future evaluations on functional longevity.

1.7 Peer reviewed paper published in scientific journal and workshop presentations

V.E. Imbayarwo-Chikosi, K. Dzama, T.E. Halimani, J.B. van Wyk, A. Maiwashe & C.B. Banga (2015) Genetic prediction models and heritability estimates for functional longevity in dairy cattle. S. Afr. J. Anim. Sci. 45 (2)

V.E. Imbayarwo-Chikosi, V. Ducrocq, C.B. Banga, T.E. Halimani, J.B. Van Wyk, A. Maiwashe & K. Dzama (2015) Impact of non-genetic factors on functional longevity of South African Holsteins. Poster presented to the 48th Congress of the South African Society of Animal Science (SASAS), 21 – 23 September 2015, Zululand, Republic of South Africa.

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Chapter 2 Literature review

Genetic prediction models and heritability estimates for functional longevity in dairy cattle
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2.1 Abstract

Longevity is a major component of the breeding objective for dairy cattle in many countries because of its high economic value. The trait has been recommended for inclusion in the breeding objective for dairy cattle in South Africa. Linear models, random regression (RR) models, threshold models (TMs) and proportional hazards models (PH) have been used to evaluate longevity. This paper discusses these methodologies and their advantages and disadvantages. Heritability estimates obtained from these models are also reviewed. Linear methodologies can model binary and actual longevity, while RR and TM methodologies model binary survival. The PH procedures model the hazard function of a cow at time ***t*** derived from survival from first calving to culling, death or censoring. It is difficult to compare methodologies for sire evaluation and ranking across countries because of the variation in the definition of longevity and the choice of model. Sire estimated breeding values (EBVs) are derived differently for the models. Sire EBVs from PH models are expressed as deviations of the culling risk from the mean of the base sires, expected percentage of daughters still alive after a given number of lactations, expected length of productive life in absolute terms or as standard deviation units. In linear, TM and RR modelling, sire EBVs for longevity have been expressed as deviations of survival from the mean estimated with Best Linear Unbiased Prediction (BLUP). Appropriate models should thus be developed to evaluate functional longevity for possible inclusion in the overall breeding objective for South African dairy cattle.

Keywords: functional longevity, proportional hazards, heritability estimates, breeding values

2.2 Introduction

In line with global trends in dairy cattle breeding, the South African dairy industry has adopted the balanced breeding concept (Banga *et al*., 2014). This entails the inclusion of all economically relevant traits in the breeding objective. Traits such as longevity, cow fertility, udder health and functional efficiency have increasingly become important in national selection objectives that were previously based on production traits alone (Carlén *et al*., 2005; Miglior *et al*., 2005; Sewalem *et al*., 2005a). The breeding objectives for South African Holstein cattle have already incorporated calving interval and somatic cell count (Banga, 2009). Recent studies (Banga *et al*., 2013; Banga *et al.,* 2014) recommend the inclusion of other traits such as live weight and longevity in these objectives.

The economic value of longevity cannot be over-emphasized as it is directly related to total herd profit and profit per day (Gill & Allaire, 1976). The trait has been reported to be the most important in South African dairy cattle, moreso for the Holstein than the Jersey breed (Banga *et al*., 2013). Length of productive life was reported to account for as much as 50% of the economic value of production traits (Jairath & Dekkers, 1994). The high economic value of longevity has been attributed to the dynamics of the trait within-herds which depend on the extent of voluntary and involuntary culling. A decrease in involuntary culling increases opportunities for voluntary culling and retention of high yielding cows for longer periods. The corresponding increases in the proportion of higher yielding mature cows and subsequent decline in the proportion of young cows allows the older cows to reach their age-dependent maximum milk yield (Vukasinovic *et al*., 2001; Strapák *et al*., 2005). This lowers costs associated with the supply of energy and protein to the young cows which require the nutrients for the attainment of physiological maturity, lactation and pregnancy. Subsequently, farmers will have better control of production costs associated with rearing and purchase of replacement of heifers as there are more heifers to sell (Van Arendonk, 1986; Forabosco *et al*., 2004; Banga *et al*., 2013).

Despite these obvious economic advantages, studies in South African dairy cattle observed a decline in longevity and other fitness traits (Banga *et al*., 2002; Dube *et al*., 2008; Makgahlela *et al*., 2008) probably because these traits were not included in dairy cattle breeding objectives in the past. To be included in the breeding objectives for dairy cattle, longevity has to be evaluated. Accurate estimation of breeding values is a prerequisite to including a trait in the breeding objective.

Different approaches have been used to estimate breeding values for longevity viz: linear, random regression (RR), threshold (TM) and proportional hazards models (PH). Linear, TM and RR models generally produce lower estimates of heritability for longevity than PH models on the original scale. Although fitting multiple trait models in linear, TM and RR methodologies estimates direct correlations between longevity and type traits, PH models can only perform univariate analysis and, therefore, are unable to give direct correlations between longevity and type traits. Instead, PH models directly determine the contribution of type traits to the risk of culling by estimating the risk ratios.

Survival analysis was first proposed for use in genetic evaluation of longevity in dairy cattle by Smith & Quaas (1984). Since then, the availability of appropriate tools and software for analysis of longevity has seen many countries rapidly including the trait in the composite selection strategy for increased production and ultimately herd profitability (Sewalem *et al*., 2005a; M'hamdi *et al*., 2010). This has, however, not been the case with South African dairy industry although there has been some research

on longevity (e.g Setati *et al*., 2004; du Toit, 2011). Du Toit *et al*. (2011) highlighted the shortcomings with the linear model approach they used for South African Jersey cattle and recommended the application of survival analysis. This paper reviews the various ways in which longevity has been defined in different studies, its economic importance in different populations and the models that have been applied for its genetic prediction. The estimates for heritability obtained in the various studies are also summarised.

2.3 Economic value of longevity

The economic value of a trait refers to the amount by which profit is expected to increase for each unit increase in the genetic merit of that particular trait holding all the other traits in the breeding objective constant (Hazel, 1943). Similarly, Vargas *et al*. (2002) defined it as a change in farm profit per average lactating cow per year, due to one unit change in genetic merit of the trait of interest. Profit can be expressed either as profit per day of herd life, profit per herd year and lifetime profit. In South Africa, Banga *et al*. (2013) reported increases in profit of between 3.59 to 3.68 ZAR and 1.09 to 2.29 ZAR for pasture raised Holstein and Jersey cattle, respectively, per day increase in longevity. Corresponding values for concentrate based systems ranged from 3.59 – 3.68 ZAR and 1.54 – 2.29 ZAR for Holsteins and Jerseys respectively. Elsewhere, Vargas *et al*. (2002) noted an increase of US$2.42 per cow per year per 1% increase in survival rate in Costa Rican Holsteins, which was within the range of US$1.35 – US$4.9 earlier reported by Visscher *et al*. (1994) for Australian Holsteins. Rogers *et al*. (1988) observed an increase in net revenue per cow per year of US$22 following a reduction of 2.9% in involuntary culling rates per year and the subsequent associated increase in longevity.

In Iranian Holsteins, economic values for longevity were evaluated by Sadeghi-Sefidmazgi *et al*. (2009) under three schemes: profit maximisation, maximum economic benefit and economic minimisation schemes. Absolute profit increased with longevity by $6.20 and $36.33 per month under profit maximisation and maximum economic benefit schemes respectively. However profits declined by $20.40 per month increase in longevity with the economic minimisation scheme.

In all the cases reported above, economic values have been reported to be very sensitive to reduction in the price of milk solids and population mean (Vargas *et al*., 2002; Banga *et al*., 2014). The positive economic values support the incorporation of longevity in the selection objective for dairy cattle as a strategy for improving selection for net economic merit.

2.4 Trait definition

Longevity or survival measures follow-up time from a defined starting point to the occurrence of a given event (Beswick *et al*., 2004; Flynn, 2012) which, in dairy, that event can be death or culling. It can either be true or functional longevity. In the former, the reasons animals leave the herd are not considered (Ducrocq *et al*., 1988). When true longevity is adjusted for production levels, it gives an approximation of functional longevity (Ducrocq & Solkner, 1998). Functional longevity therefore is the ability of an animal to delay involuntary culling i.e. the ability of the cow to avoid culling for reasons other than milk production. This indicates the health, fertility and overall fitness of an animal (Bünger & Swalve, 1999; Zavadilová & Štípková, 2012) and is therefore of particular interest to the breeder (Vukasinovic, 1999). Many measures of functional longevity have been proposed, *viz*: age, number of lactations, length of productive life and lifetime production at time of cow disposal (Ducrocq *et al*., 1988).

Longevity has assumed different trait definitions (Vollema & Groen, 1997; Brotherstone *et al*., 1998) all of which are based on age at culling or death (uncensored) or censoring and survival to a given age or predetermined period within or across lactations (Jamrozik *et al*., 2008; Forabosco *et al*. 2009). It has been scored as a binary trait (e.g. Ajili *et al*., 2007; Holtsmark *et al*., 2009; du Toit, 2011) in which animals are scored on the basis of whether or not they survived up to a specific time, age or event and analysed with either linear (e.g Du Toit *et al*., 2009) random regression (e.g. Veerkamp *et al*., 2001; van Pelt & Veerkamp, 2014) or threshold models (e.g. Boettcher *et al*., 1999; van der Westhuizen *et al*., 2001; Holtsmark *et al*., 2009). The survival period could be limited to either within lactation (e.g. Holtsmark *et al*., 2009) or across all lactations (e.g. Caraviello *et al*., 2004a & 2004b; M'hamdi *et al*., 2010). This definition is constrained by the fact that only animals with an opportunity to survive the entire specified period can be used in genetic analysis whilst excluding records from the most recent animals. Besides, cows that are culled or where recording ended before the specified time are usually considered missing and excluded from analysis (Veerkamp *et al*., 2001).

In South Africa, longevity in Holstein cattle was defined as number of lactations initiated among dairy (Setati *et al*., 2004) whilst Maiwashe *et al*. (2009) and van der Westhuizen et a. (2001) considered longevity in South African beef cattle as stayability defined as the probability that a cow reached a specific age given the opportunity to reach that age. Du Toit *et al.* (2009) treated survival in South African Jersey cattle as a binary trait and defined it as survival to the next lactation, determined on the basis of whether an animal had a subsequent lactation or not. Survival in a given lactation was coded 1 if the cow survived that lactation, 0 if the cow was culled during that lactation or if the number of days between the current calving and extraction date exceeded 581 days.

Sewalem *et al*. (2005b) and Holtsmark *et al*. (2009) variably defined longevity as herd life in the first lactation or the first five lactations calculated as the number of days from calving to either culling, death or censoring, survival scores for lactations 1 to 5 and survival to 365 days after first calving after which an animal was scored 0 if the cow was culled before the 365 days and 1 otherwise. Tsurunta *et al.* (2005) defined longevity as the total number of lactation days up to 84 months of age with restrictions of ≤305, 500 or 999 days per lactation as well as number of days from first calving date to the last culling date including dry periods. Elsewhere, longevity was defined as functional herd life (e.g. Chirinos *et al*., 2007) which is the herd life of a cow adjusted for individual milk yield relative to milk production of the entire herd. Table 2.1 shows the different trait definitions that have been adopted for national genetic evaluation of dairy cattle for longevity by countries on the Interbull.

2.5 Modeling survival data

2.5.1 Nature of survival data

Longevity manifests itself as a threshold trait. Such traits show distinct categorical phenotypes and their expression is not continuous. Inheritance of such traits is based on the fact that they have an underlying continuous distribution with a threshold, which imposes a discontinuity on the visible expression of the trait (Falconer & Mackay, 1996). When plotted, longevity data are characteristically skewed to the left because a larger proportion of cows are in early lactations (Caraviello *et al*., 2004b). Of significance is that environmental factors that influence an animal's risk of being culled at any given time may differ dramatically on the basis of the prevailing conditions and will most likely change throughout its lifetime (Caraviello *et al*., 2004a; Zavadilová *et al*., 2011; Flynn, 2012) rendering the factors time-dependent. At any instance, survival data will have both complete and incomplete records. Events like culling and death may be known to have occurred and will therefore be uncensored. At the same time, animals may have been lost to follow-up and events like culling or death not known to have occurred. These animals may also still be alive at time of analysis in which case only the lower bound of their productive life will be known. Such records cannot be excluded from evaluation of survival as this might lead to bias and are therefore censored (Beswick *et al*., 2004). Appropriate modeling strategies for such data should accommodate these unique characteristics without loss of important phenotypic, additive and environmental variance information necessary for genetic evaluation (Weigel *et al*., 2003).

2.5.2 Models for analysis

Linear, threshold, random regression and proportional hazards models have all been used in genetic evaluation of animals for functional longevity. Table 2.1 shows the different models used for national genetic evaluations of survival depending on the definition of the survival trait by country. As of 2014,

Table 2.1 Trait definition and models used by countries in Interbull

Country	Reference year	Parities evaluated	Trait definition	Model(s)
Australia	2004	7 yrs post 1st calving	Probability of surviving from one year to the next – binary trait Combined longevity	Animal model
Belgium	2010	1 – 5	Survival over successive lactations	RR survival animal model
Canada	2009	1 – 3	Expected differences among daughters in days.	5-trait animal model
Czech	2013	All parities	Functional longevity measured as number of days from 1st calving to culling or to actual date	ST S-MGS model – Weibull
Denmark, Finland, Sweden	2010	1 – 5	1st to 5th year longevity measured as days survived to end of that lactation	MT–BLUP- AM (5 traits)
France	2012	1 – 5	Functional longevity Combined longevity	ST S-MGS model – Weibull MT BLUP AM
Germany, Austria and Luxemboug		All parities	Functional longevity measured as number of days from 1st calving to culling or to actual date	ST S-MGS model - Weibull
Great Britain	2005	1 – 5	Lifespan score computed from number of lactations completed up to the 5th lactation.	BLUP Bivariate Animal model
Hungary	2011	1 – 10	Functional longevity of cow in days.	S-MGS - Weibull
Ireland	2013	1 – 6	Survival to the next lactation	MT-BLUP-AM
Israel	-	All parities	Functional longevity from 1st calving to culling (within 8 years) in days	ST BLUP-AM
Italy	2011	All parities	Functional longevity of cow in days	ST S-MGS model - Weibull
Netherlands	Unknown	All parities	Functional longevity of cow in days	ST S-MGS model – Weibull
New Zealand	2013	1 – 5	Functional longevity from 1st to 5th lactation Combined longevity since 1987	MT-ML-BLUP-Animal Model
Poland	2014	All parities	Functional longevity measured as number of days from 1st calving to culling date or last known test date	ST Sire model - Weibull
Slovenia	2013	1 – 6	Functional longevity measured as number of days from 1st calving to culling or to the moment of data collection or till the end of 6th lactation	ST S-MGS model – Weibull
South Africa	2013	1 4	Differences in functional herd life of daughters over defined periods.	MT-BLUP-AM
Spain	2013	1 – 5	Functional longevity, Indirect Functional Longevity Combined longevity	ST S-MGS model – Weibull
Switzerland	2008	1 – 6	Productive life span of cow measured in days Combined longevity	ST S-MGS model, Weibull
USA	-	All parities	Productive life measured as time in herd before culling or death.	ST BLUP-AM

MT-BLUP-AM – Multiple Trait BLUP- Animal Model; ST S-MGS – single trait sire maternal grand sire model; RR – Random regression (Interbull, 2014)

of the 20 countries on Interbull that were evaluating longevity at national level, more than 50% used survival analysis including France, Netherlands, Spain, Germany, Czech Republic and Hungary. These used sire-maternal-grandsire models whilst Poland and Italy used the sire models in Polish Holstein-Friesian and Brown Swiss cattle respectively (Interbull, 2014). A sizeable number of countries were using the linear models in which survival is usually evaluated in either a single or multi-trait analysis with animal, sire, maternal-grandsire or sire-maternal-grandsire survival models (Holtsmark *et al*., 2009).

Survival in South African Holstein, Jersey, Guensey and Ayrshire cattle was evaluated using a multiple-trait BLUP animal model with survival traits defined as survival up to 120 days in milk in the first lactation, survival to 240 days in milk in the first lactation, survival up second calving, survival up to third calving and survival up to fourth calving Setati et al., 2004; du Toit, 2011). Until 2006, genetic parameters for functional longevity in Japanese dairy cattle were estimated using a linear multi-trait animal model with direct effects of milk yield and seven conformation traits (Sasaki *et al*., 2012). Other countries such as Australia, Canada, Ireland and New Zealand used a multi-trait linear animal model to evaluate longevity in all dairy breeds. Great Britain used a bivariate animal model for all breeds whilst the USA and Israel evaluated longevity with a single trait BLUP animal model for all breeds. Belgium is the only country that used random regression lactation survival animal models to evaluate longevity (Interbull, 2014).

Modeling survival for genetic evaluation of functional longevity has therefore not been standard across the different countries. These variations in modeling methods imply that sires cannot be compared and ranked across countries although this largely depends on the correlation between these differently defined traits. Researchers are therefore unable to conclusively identify the better of multiple-trait, threshold, proportional hazards and random regression models since the models give different rankings of animals. As a consequence, there is no universal system for sire evaluation and comparison as is the case with production traits (Sewalem *et al*., 2005b).

2.5.2.1 Linear models

Linear animal and sire models have been used by a number of researchers to evaluate survival (e.g. Caraviello *et al*., 2004a; Holtsmark *et al*., 2009; du Toit, 2011; Zavadilová & Štípková, 2012). In these analyses, indicators of longevity such as whether the animal was still alive at a particular time or at the beginning of a given lactation period have been discussed and used (Vukasinovic, 1999; Holtsmark *et al*., 2009;). A value of time ***(t)*** on a time scale is decided upon and the record of each animal converted into a 0 or1 trait depending on whether the animal is alive at time ***t*** or not. Longevity

in this case is considered a binary trait, the analysis of which, excluding fixed effects, is based on the model:

$$y_{ij}(t) = \mu + s_i + e_{ij} \qquad \text{(i)}$$

where $y_{ij}(t)$ is 0 if the j^{th} progeny of sire ***i*** is not alive at time ***t***, and 1 otherwise; μ is the population mean; s_i is breeding value of sire ***i*** on the binary scale and e_{ij} are random residuals.

Linear modeling of binary survival has been carried out in Canadian Holsteins (Boettcher *et al*., 1999), Czech Fleckvieh (Zavadilová *et al*., 2009), Norwegian Red (Holtsmark *et al*., 2009), South African Jersey cattle (du Toit, 2011), Italian Brown Swiss (Samoré *et al*., 2010) and others (e.g. Jamrozik *et al*., 2008; Zavadilová & Štípková, 2012). Linear models have also been used to analyse survival based on actual and projected records, using currently available information (VanRaden & Klaaskate, 1993). Models have been developed for projecting the herd life of cows that would be still alive at time of analyses (e.g. Brotherstone *et al*. 1998; Caraviello *et al*., 2004a; Zavadilová & Štípková, 2012) and then applying linear models to the combined data sets with the actual and the projected herd life.

The major advantage of linear modeling is its relative simplicity (Boettcher *et al*., 1999) and, as demonstrated by a number of researchers (e.g. du Toit, 2011), its ability to run either a univariate or a multi-trait analysis with an animal, sire, maternal or maternal grand-sire model, which is not possible with proportional hazards modeling. The major criticisms of linear models are that they make many incorrect assumptions that the true survival times are continuous and yet they are not necessarily normally distributed (Yazdi *et al*., 2002). Many different reference times can be chosen leading to loss of substantial information. Besides, animals culled or dying one day or one year before the reference time are all treated the same leading to incorrect evaluation of animals (Ducrocq *et al*., 1988). Furthermore, survival times are derived from a product, rather than a sum of time dependent and independent factors that influence longevity (Beilharz *et al*., 1993; Vukasinovic, 1999) such that if at least one of these factors is compromised, then the longevity of an individual animal will also be affected (Ducrocq & Skolner, 1998). This reduces the applicability and value of linear models in estimating genetic parameters for survival. Linear models do not render themselves appropriate for analysis of binary traits as much as they do for continuous variables such as milk production traits (Boettcher *et al*., 1999) since the distribution of binary traits is discontinuous and therefore categorical. Analysing such data with linear procedures on the assumption of continuous phenotypic distributions ignores the non-continuous nature of threshold traits. According to Gianola

(1982), the main objection to using BLUP with categorical data is that breeding values and residuals obtained from their use are not independent of each other.

Since the variable of interest is time to death, culling or censoring, when data is analysed, culling or death may not have occurred for some animals. Where these events have occurred, there is need to assess the effect of independent variables on the variable of interest which, again is not easily accomplished through linear models. Furthermore, linear models assume that non-genetic factors influencing the time to culling or death have a constant effect throughout the entire life of the animal. The conditions that animals are exposed to are time-dependent. Neither can linear models optimally account for time-dependency of variables nor non-linearity in data (Vukasinovic, 1999; Caraviello *et al*., 2004a; Zavadilová *et al*., 2011). Nevertheless, linear models have been used to evaluate binary survival and absolute longevity in a number of studies (e.g. Tsurunta *et al*., 2005; Zavadilová *et al*., 2009; du Toit, 2011).

2.5.2.2 Random regression survival animal models

Although random regression models were introduced by Henderson (1982) and Laid & Ware (1982), it was not until 1994 that Schaeffer & Dekkers (1994) proposed their use for analysis of test day production records in dairy cattle breeding and 1999 when Veerkamp *et al*. (1999) proposed their use for evaluation of survival through longitudinal generalisation of the multiple trait models. In random regression modeling, binary observations are assigned to each discrete unit in the cow's lifetime, e.g. per lactation or per month after first calving, and a linear model with random regressions for an animal genetic effect can then be fitted to this data in genetic evaluation. Breeding values are estimated for both cows and sires and for each point on the trajectory (Jamrozik *et al.,* 2008). Linear regression of observations of the trait under consideration on indicator variables is performed with the animals' additive genetic effects fitted as random effects. Since functions of time such as days in milk can easily be modelled within the mixed model framework (Henderson, 1982), trajectories can be described. The covariables are usually nonlinear functions relating time to the traits. Fitting sets of random regression coefficients for each individual random factor (*e.g.* additive genetic and permanent environmental effects) produces the estimates of the corresponding trajectories (Dzomba *et al*., 2010). The univariate random regression model can be extended to survival analysis and, for example, presented as proposed by Schaeffer (2004):

$$y_{ijklmno:t} = (YS : Ht)_{ij} + (YSAP:t)_{ikl} + r(a,x,m1)_n + r(pe,x,m2)_k + e_{ijklmno:t} \qquad \text{(ii)}$$

where $y_{ijklmno:t}$ is the n^{th} observation on the k^{th} animal at time t belonging to the i^{th} fixed factor and j^{th} group; YS is the i^{th} year-season of first calving, H is the j^{th} herd, A is the k^{th} age at first calving group,

P is the l^{th} production level as a deviation from herd average in first lactation, $r(a, x, m1)_k = \sum_{l=0}^{m_1} a_{kl}\, x_{ijk:l}$ is the notation adopted for random regression function where a would denote the additive genetic effects of the k^{th} animal, ***x*** are appropriate orthogonal polynomials of time, ***t***, after first calving, ***a*** are the random regression coefficients for additive genetic value of animal ***n***, ***pe*** are the random regression coefficients for permanent environmental effects of animal ***n*** and $e_{ijklmn:o}$ is the residual effect.

The basic idea underlying random regression models consists of modeling the additive genetic values as a function of an observed dependent variable through a set of random coefficients. Models used in genetic evaluation of animals through random regression involve continuous functions to describe both the fixed and random effects. The EBVs are then predicted by continuous functions of deviations from each animal, considered random, in relation to average curve, considered fixed (Mota *et al*., 2013). Random regression models have been used in dairy cattle breeding to evaluate production traits (e.g. Jamrozik & Schaeffer, 1997; Mrode & Swanson, 2004) and other traits such as mastitis and fertility traits (e.g. Carlen *et al.,* 2005; Tsurunta *et al*., 2009), conformation, body condition scores, feed intake, heart girth measures (Schaeffer, 2004) and survival (Jamrozik *et al*., 2008).

Random regression models can generate sire and dam proofs for survival for each point on the trajectory. They are relatively more robust to censoring data (Veerkamp *et al*., 1999) and have a direct link with both proportional hazards and generalized linear models. Random regression models can handle time-dependent fixed effects and offer scope for the possibility of using multiple trait analysis of yield, functional traits and survival (Veerkamp *et al*., 2001). Furthermore, they can handle random animal effects unlike proportional hazards models. The number of distinct genetic effects per animal can be optimized and it should be straightforward to estimate genetic and environmental correlations with other predictors of longevity, e.g. linear type traits (Brotherstone *et al.,* 1998; Jairath *et al.,* 1998). When compared with the multi-trait linear models approach to analysis of survival data, random regression models have the advantage that fewer parameters are required to explain the genetic variation in lifespan (Veerkamp *et al*., 2001).

The applicability of random regression models in animal breeding have, however, been limited due to problems associated with the large number of parameters to be estimated and poor polynomial approximations. Because of this, random regression models the need to analyse very large data sets leading to implausible estimates at the extremes of trajectories and associated high computational requirements (Dzomba *et al*., 2010). Besides, in extremes of the age range or when data are insufficient, the estimated parameters may not be accurate (Meyer, 1999). By treating binary

data as if it were continuous and assuming uncorrelated normally distributed residuals in each lactation, the procedure ignores the effect of repeated records. More appropriate error structures would, therefore, be required (Veerkamp *et al*., 2001).

2.5.2.3 Threshold models

These include simple threshold models (TM), sequential threshold models (STM), threshold repeatability models (TRM) and threshold cross-sectional models (TCM). In threshold modeling, survival is considered a binary trait just as in some cases of linear modeling (i.e. 0=alive at time t and 1= dead at time t) only that threshold models are based on the probit model. The probit model hypothesises that a linear model with a nonlinear relationship between the observed and underlying scale describes an underlying variable refered to as the liability (Gianola and Foulley, 1983). There is therefore a generalized linear model that is linked to the binomial trait (survival in this case) with a probit link function. Threshold models have been used in evaluating survival to weaning in pigs (Cecchinato *et al*., 2010), reproductive traits in South African beef cattle (van der Westhuizen *et al*., 2001) and dairy cattle survival (Holtsmark *et al*., 2008; Holtsmark *et al*., 2009). Holtsmark *et al*., 2009 evaluated survival within the first five lactations of Norwegian Red dairy cattle using a threshold repeatability model (TRM), assuming a probit link function, and the threshold cross-sectional probit link model (TCM). Survival in the study was scored 1 if the cow had a calving **k + 1**, 0 if the cow was culled in lactation **k** and missing if the cow was culled before the lactation or if recording period ended during lactation **k**. Animals that were culled on the same day they calved were given a herd life of 1.

Sequential threshold models (STM), described by Albert & Chib (2001), have also been used to analyse the number of lactations per cow, functional discrete-time survival, that occur in sequential order (Gonzalez-Recio & Alenda, 2007; Holtsmark *et al*., 2009). The STMs are based on the principle that for an observation to be present in a given lactation it must have survived through all previous lactations. This means that for any observation at a given stage, it is necessary that the animal should have passed through all previous stages (Gonzalez-Recio & Alenda, 2007) and by implication, the method accounts for what occurred in the previous stages thereby increasing reliability of the estimates obtained. This approach can describe the physiological or decision processes that occur in a sequential order and the model can also handle large data sets. Sequential modeling, unlike proportional hazards modeling, is capable of using an animal model but this increases computation time. Furthermore, sequential threshold models can accommodate time-dependent covariates and censoring (Gonzalez-Recio & Alenda, 2007; Cecchinato *et al*., 2010). Together with threshold models, they have been used to evaluate survival in dairy cattle (Gonzalez-Recio & Alenda, 2005).

The major drawback of threshold models is that the heritability estimates obtained from these models are from an underlying scale yet the observed phenotypes are on the same scale as that for linear models. As such, selection on the EBVs from the threshold models would not produce improved genetic progress on the observed scale than selection on EBVs from linear model (Boettcher *et al*., 1999). Further studies are however needed to improve knowledge on the behaviour of STM.

2.5.2.4 Proportional hazards (PH) models

The use of PH models in dairy cattle breeding was initially suggested by Smith & Quaas (1984) and is now widely accepted for analysis of functional longevity in dairy cattle (e.g. Caraviello *et al*., 2004a; Caraviello *et al*., 2004b; Mészáros *et al*., 2008; Durr *et al*., 1999; M'hamdi *et al*., 2010; Jovanovic & Raguz, 2011). More than 50% of all member countries of Interbull evaluating longevity now use PH models with sire or sire-maternal grandsire models, although some countries such as New Zealand, Ireland, Australia, Great Britain and USA still use the multi-trait animal or sire models for evaluation of functional longevity (Potocnik *et al*., 2009; Interbull, 2014). Proportional hazards models are based on modeling the survival function i.e. the probability that an animal survives past a specified time t; and the hazard function i.e. the instantaneous rate of failure (Ducrocq, 2005). These two functions can differentiate between a cow that died at exactly time ***t*** and a cow that was last seen alive at time ***t*** but may have survived several additional months or years. The PH model is based on the assumption that the hazard rate or risk is a product of a time-dependent baseline hazard and an exponential function of a series of explanatory variables, covariates (Ducrocq, 1997; Rao & Schoenfeld, 2007). Proportional hazards models assume that the covariates have a multiplicative effect on the baseline hazard rate. This implies that the ratio of the hazard rates of any two animals observed at any time ***t*** associated with any set of covariates will be a constant with respect to time and proportional to each other and as such, the model is referred to as the PH model (Kumar & Klefsjo, 1994).

These models do not always give the highest fit with current data yet they are expected to accurately estimate the performance of future offspring of a sire (Holtsmark *et al*., 2009). Furthermore, they assume that survival is the same trait throughout the entire life of the animal yet correlation between longevity in lactations one to three has been shown to be less than one implying that it, in fact, is not one trait throughout life. Unlike linear models, PH models cannot account for non-random mating among animals (Jairath & Dekkers, 1994; Boettcher *et al*., 1999). Besides, the commonly used software for survival analysis with PH models currently only use univariate analyses (Veerkamp *et al*., 2001; Holtsmark *et al*., 2009) and therefore unable to adjust for correlations between traits, a pre-requisite for increased accuracy of evaluation of animals. Since there are no multivariate analyses, it is difficult to use indicator traits to estimate longevity early in life as most important

information during early life comes from predictor traits (Brotherstone *et al*., 1998). This is unlike other software that employ linear and threshold modeling which can use multivariate analyses thereby adjusting for correlation among traits during genetic evaluation of animals. Another limitation of PH modeling in dairy cattle is related to the software currently available for use, the survival kit. The software is not able to process full animal models (Holtsmark *et al*., 2009) restricting analyses to sire and sire maternal grandsire models. This ignores contribution of the cows mated to these sires to production performance of the daughters especially when there is assortative or disassortative mating. Although PH models are considered optimal in a statistical sense, they in fact may not be economically optimal (VanRaden *et al*., 2006).

Despite the limitations associated with this approach, proportional hazards models have become the method of choice for analysing survival data. Due to their ability to handle censored data, appropriately accommodate the non-normal distribution of survival data as well as the ability to incorporate time-dependent environmental effects in the model (Caraviello *et al*., 2004b). Moreover, just like the mixed linear models, PH models can be adapted to include random genetic effects (Ducrocq, 1997) in which case such mixed survival models are referred to as frailty models. The commonly used proportional hazards models in cattle evaluations are the semi-parametric, based mainly on the Cox model, and the parametric, dominated by the Weibull models. The semi-parametric model does not assume any distribution for the baseline hazard, whilst the latter assumes that the baseline hazard function follows a specified distribution (Rao & Schoenfeld, 2007). Weibull models have several advantages over Cox models. They allow stronger inferences about the survival times to be made than Cox models. The output from the Weibull model relates directly to duration of survival thereby allowing inferences to be made about the true event. Moreover, Weibull models also incorporate non-constant hazard functions unlike the Cox models which assume that the risk of an event remains constant throughout time (Flynn, 2012). However, the Cox model is much more flexible since the hazard function is not restricted to any specific form. Although the Cox models simultaneously explore the effects of several covariates on longevity and allow the isolation of the effects of these covariates, the Weibull model further assumes that the baseline hazard function, $\lambda_0(t)$, can be parameterised according to a specific model for the distribution of the survival times (Walters, 2009).

2.5.2.5 Model comparison

Statistically, it is difficult to compare results from models for binary data, such as threshold and random regression, with models for continuous data e.g. linear models, because the numeric scales for these models are different (Littell *et al*., 1996; Matos, 1997). The link functions and the distribution functions that are assumed for the response trait are also differ for PH, threshold, linear and random

regression models. Precisely, the different link functions contribute to the problem of comparing mathematical models in different numeric scales. However, some comparisons based on procedure and outcomes have been carried out. Linear models are very simple to implement and generally require the least computing resources, although they have been reported to be the least statistically appropriate models for categorical and censored data. By contrast, threshold models were found to be more appropriate for binary survival than linear models, (Boettcher *et al*., 1999).

In a simulation study, Jamrozik *et al*. (2008) compared the proportional hazards, multi-trait linear and the linear random regression models. It was noted that the Weibull model was relatively better than both linear and random regression models for genetic evaluation of dairy cattle for functional longevity, i.e. time of culling within the interval 1 to 100 months post first calving. In terms of correlation between the true and the estimated breeding values, the proportional hazards model using the Weibull was the most accurate followed by random regression model evaluations. However, random regression models demonstrated the greatest predictive abilities than the Weibull and multi-trait linear models for overall survival (influenced by health, fertility and production). Comparison between the predictive abilities of sire EBV from Weibull frailty sire model and the linear animal model for survival up to second, third, fourth and fifth lactation, none of the models were significantly superior to the other although the Weibull tended to perform somewhat better than the latter (Caraviello *et al*., 2004a).

When comparing the general threshold and linear multi-trait models, Holtsmark *et al*. (2009) obtained the best performance of sire EBVs from linear multi-trait models. Sire EBVs from linear cross-sectional and threshold cross-sectional models performed similarly to those obtained by linear repeatability models and threshold repeatability models. Sire EBVs from Weibull frailty models with data from first lactation only performed better than Weibull frailty models with data from lactation one to five, linear repeatability model as well as threshold repeatability models. This was probably because linear repeatability, threshold repeatability and the Weibull frailty models for lactation one to five assumed genetic correlation of unity between survival in different lactations. Results from previous studies (e.g. Boettcher *et al*., 1999; Sewalem *et al*., 2007) indicated that because of the genetic correlations below unity for survival in first and later lactation, survival in first lactation was a distinct trait from survival in later lactations. Boettcher *et al*. (1999) found high correlations of up to 0.98 between sire EBV from the linear and threshold sire models in Canadian Holsteins and up to 0.90 between sire EBVs from proportional hazards models, sire animal models and threshold models. These results were consistent with earlier estimates from Meijering & Gianola (1985) and Weller & Ron (1992) implying that the trait in linear sire model and threshold models was similar to the survival trait in proportional hazards modeling of survival for 305-day lactation records. Although

linear multi-trait and random regression models are used for binary traits, they are not optimal in terms of statistical correctness (Jamrozik *et al.,* 2008) regardless of the fact that Meijering & Gianola (1985) reported no practical differences in rankings of individual animals from either a linear or a threshold model when traits were binary.

2.6 Heritability estimates

Heritability estimates for survival traits have been expressed differently for the different models. Unlike estimates obtained with linear, threshold and random regression sire models, estimates from proportional hazards models have been expressed in different studies as either on a log linear scale, original scale or as effective heritability (Yazdi *et al*., 2002). Heritability estimates obtained from linear sire models have been found to be generally lower than those from threshold sire models. Table 2.2 shows heritability estimates for longevity estimated with proportional hazards sire, random regression, threshold and linear animal and sire models.

2.6.1 Linear models

Linear models have been reported to produce generally lower estimates of heritability for longevity than PH models, suggesting increased accuracy of selection from the latter (Boettcher *et al*., 1999; Ducrocq, 2002; Roxstrom *et al*., 2003; Sewalem *et al*., 2005b). du Toit (2011) reported heritability estimates in the range of 0.01 to 0.03 in South African Jersey cattle with both sire and animal models, in a multivariate linear model analysis of length of productive life as binary trait. Setati *et al*. (2004) had reported slightly higher estimates of 0.06 for South African Holsteins, using a bivariate linear animal model. Zavadilová *et al*. (2009) reported estimates of about 0.05 with linear animal model in Czech Fleckvieh whilst Tsurunta *et al*. (2005) found estimates of 0.08 to 0.10 in American Holsteins with a linear animal model using Gibbs sampling. Generally, these heritability estimates ranged from as low as 0.01 to as high as 0.20 depending on the type of linear model adopted. Despite this wide variation, Holtsmark *et al.* (2009) pointed out that the heritability estimates for survival as a binary trait, obtained with linear models, were frequency dependent and as such, heritability values from different studies could, therefore, not be compared directly.

2.6.2 Random regression models

Van Pelt & Veerkamp (2014) estimated genetic parameters for longevity in Dutch dairy cattle using random regression models. Models used records of monthly survival up to 72 months from first calving and heritability estimated for monthly survival were estimated. If animal survived to month ***i*** + 1, it was considered alive and scored 100 and those culled in month ***i*** were considered dead and scored 0. Using a sire-maternal-grandsire (S-MG) model, heritability estimates for monthly survival ranged between 0.002 and 0.011 with higher estimates of heritability for the later periods and the

cumulative heritability for the entire 72 months was 0.146. These estimates for monthly survival were lower than estimates of 0.016 to 0.181 reported for national evaluations (Forabosco *et al*., 2009) and estimates of 0.01 to 0.07 from an earlier study by Veerkamp *et al*. (2001) with random regression models in British dairy cattle. Estimates from van Pelt & Veerkamp (2014) were also significantly lower than estimates of 0.12 – 0.36 obtained from Canadian Simmental beef cattle using random regression models (Jamrozik *et al*., 2008). Such huge discrepancies could be defined within the scope of different trait definitions of longevity in beef and dairy cattle. Generally, however, random regression models produce lower heritability estimates than PH models.

2.6.3 Threshold models

Heritability for longevity has been estimated with threshold models in Canadian Holsteins (Boettcher *et al*., 1999), Spanish Holsteins (Gonzalez-Recio & alenda, 2007), South African beef cattle (van der Westhuizen *et al*., 2001), South African Angus cattle (Maiwashe *et al*., 2009), Norwegian Red (Holtsmark *et al*., 2009) and Brazilian Holsteins (Kern *et al*., 2014). Heritability estimates in dairy cattle breeds were generally low, ranging from 0.04 (Holtsmark *et al*., 2009) to 0.15 (Kern *et al*., 2014). Estimates in beef cattle breeds were however higher, ranging from 0.08 (van der Westhuizen *et al*., 2001) to 0.30 (Maiwashe *et al*., 2009) probably due to differences in trait definition between dairy and beef cattle. Heritability estimates obtained with a sequential threshold model were slightly higher at 0.11 (Gonzalez-Recio & Alenda, 2007) than those obtained for dairy cattle with threshold models. As expected STM are known to increase reliability by accounting for what may have occurred in the previous stages. Estimated respective heritability estimates within lactation one and across lactation to lactation were also found to be low but significantly higher than estimates obtained with linear models (Holtsmark *et al*., 2008; Holtsmark *et al*., 2009). This was despite the different definitions used for longevity in the studies. Earlier studies observed that if functional longevity was expressed as a binary trait, the difference in heritability estimates obtained from the underlying scale was negligible when either linear or non-linear models were used. Generally, theoretical and empirical results indicate higher estimates of heritability from threshold models than from linear models (Boettcher *et al*., 1999).

2.6.4 Proportional hazards models

Heritability estimates for functional longevity have been obtained and expressed on either an original or logarithmic scale with PH models. Ducrocq & Casella (1996) defined heritability on the logarithmic scale and modified under simulation to incorporate the tri-gamma function (γ) as used by Sasaki *et al*. (2012) and Terawaki & Ducrocq (2009). The estimates of heritability on a logarithmic scale were deficient in terms of biological interpretation and were also reported to have a weak relationship with reliabilities for the genetic evaluations (Ducrocq, 1999). Ducrocq (1999) transformed heritability on

log scale to the original scale (h_o) using the Taylor series expansion and found this to provide good results for reliability of genetic evaluations, for situations in which the Weibull parameter relating to shape of the distribution (ρ) was close to two. Large biases were, however, obtained if this ρ was less than or close to one (Chirinos *et al*., 2007). The heritability on the original scale has one major advantage over the logarithmic scale estimates though. It gives good approximations of the true prediction error variance of the bulls based on survival of their offspring. However, as a limitation, it estimates heritability using one of the two Weibull parameters, the shape parameter (ρ) and the scale parameter. These two parameters have a relatively strong negative correlation, implying that different combinations of the two parameters can lead to similar fit of the data but producing different heritability estimates (Yazdi *et al*., 2002). Moreover, the derivation and interpretation of the obtained heritability on original scale has, in some research, been considered dubious. Because of these limitations, Yazdi *et al*. (2002) developed an alternative formula for computation of the heritability under a normal Weibull proportional hazards model expressed as effective heritability. This has been modified and extended for use in different situations (e.g. Bünger *et al*., 2001; Roxstrom *et al*., 2003) because it accounts for censoring unlike original and logarithmic heritability. Effective heritability calculates expected reliabilities of estimated breeding values as a function of the expected number of animals with censored records at any given time (Mészáros *et al*., 2010).

Generally, the heritability for survival estimated on the original scale has been reported to be higher than estimates obtained on log linear scale, the latter of which are consistent with estimates from linear models (Ducrocq & Skolner, 1998). Heritability estimates on a log linear scale, range from 0.05 to 0.10 (Caraviello *et al*., 2004b) whilst on average, they range between 0.15 to as high as 0.20 when determined on the original scale (Caraviello *et al*., 2004a). Using the Weibull proportional hazards models, Mészáros *et al*. (2008) reported heritability estimates of 0.05 on logarithmic scale in Croatian Pinzgau cattle. This concurred with the logarithmic estimates of 0.04 earlier reported by Van der Linde *et al*. (2006) and Chirinos *et al*. (2007). However, these were much lower than earlier estimates of 0.161 to 0.217 (Ducrocq, 1997), 0.12 (Egger-Danner *et al*., 2005) as well as 0.21 and 0.22 respectively for true productive life and functional productive life on the original scale (Bünger & Swalve, 1999). The wide variation in heritability estimates for animals in different regions and countries, just like in linear modeling, can be attributed to differences in the magnitude of the genetic variation in cow longevity between the regions although this could also be due to differences in the accuracy of sire identification, record keeping (Caraviello *et al*., 2004b) and the precision of data analyses. Table 2.2 shows some heritability estimates for survival obtained with different models

2.6.4.1 Survival and hazard functions

The survival function is estimated as the probability of survival of cows from observed survival times, both censored and uncensored, using non-parametric methods as described by Clark *et al*. (2003). The survival function, S(t), for the cows is determined through the Kaplain-Meir (KM) method and has been defined as the probability that an animal survived past time **T.** i.e.

$$S(t) = Prob(T \geq t) = 1 - Prob(T < t) = 1 - F(t)$$

Where **F(t)** is be the cumulative probability density function describing the probability that an animal will be culled or dead at time **t** or generally the failure function with a density function **[f(t)].** Through the KM method, the PROC LIFETEST procedure S(t) can be estimated as: -

$$\hat{S}(t) = \prod_{t_s \leq t} \left(1 - \frac{d_j}{n_j}\right)$$

where: $\hat{S}(t)$ is the survival function;

d_j is the number of cows culled/dead at time t_j;

n_j is the number of cows still alive at t_j and are therefore still at risk for experiencing culling or death

From the obtained S(t), the probability distribution function, f(t), is estimated as follows (Ducrocq, 1997): -

$$f(t) = \lim_{\partial \to 0} \frac{Prob[t \leq T \leq t + \Delta t]}{\Delta t} = \frac{dF(t)}{dt}$$

The KM method can also test for equality of the estimates of the survival function of two or more different populations and appropriately determine the adequacy of the predicted survival. The choice of model to use in survival kit (Weibull or Cox model) is determined by the shape of the plot of log [-log S(t)] against log(t) (Ducrocq, 1994). If the resulting graph is linear, then the assumptions of the parametric Weibull distribution holds (Carlen *et al*., 2005) and the Weibull proportional hazards model can be applied in survival analysis.

The probability of a cow being culled at time *t* given it was alive just before time *t* (i.e. t-1), known as the hazard function, and relative risk ratios are estimated from f(t) and S(t) as adapted from Ducrocq (1997): -

$$\lambda(t) = \lim_{\partial \to 0} \frac{Prob[t \leq T \leq t + \Delta t \mid T > t]}{\Delta t} = \frac{f(t)}{S(t)}$$

Table 2.2 Heritability estimates for functional longevity obtained with linear, random regression, threshold and Weibull Proportional hazards models

Breed	Number of records	Method	Model	Trait	h^2	Reference
Brazilian Holsteins	-	Threshold model	AM	SGA	0.09 – 0.15	Kern *et al*., 2014
British Holsteins	24 741	Random regression	AM	FL	0.01 - 0.07	Veerkamp *et al*. (2001)
Canadian Simmental	1 164 319	Random regression L&T	AM	Stayability	0.12 – 0.36	Jamrozik *et al*. (2001)
Canadian Holsteins	700 000	Threshold	SM	FL	0.07	Boettcher *et al*. (1999)
Czech Fleckfieh	58 493	Linear models,	AM	FL	0.05	Zavadilová *et al*. (2009)
Czech Holsteins	57 803	Linear bivariate	AM	NL	0.05	Zavadilová &Stipkova (2012)
Czech Holsteins	57 803	Linear bivariate	AM	NLF	0.04	Zavadilová &Stipkova (2012)
Czech Holsteins	57 803	Linear bivariate	AM	LPL	0.03	Zavadilová &Stipkova (2012)
Dutch dairy cattle	950 616	Random regression	SMG	FL	0.002 – 0.011	van Pelt & Veerkamp, 2014
French Holsteins	629 716	Weibull PH	SM	FL	0.217	Ducrocq (1997)
French Holsteins	8 682 630	Weibull PH	SMG	FL	0.108	Ducrocq (2005)
Japanese Holsteins	158 719	Weibull PH	SM	FLPL	0.046 – 0.102	Terawaki & Ducrocq (2009)
Japanese Holsteins	117 404	Weibull PH	SM	HL	0.119 – 0.123	Sasaki *et al*. (2012)
Norwegian Red	808 750	Weibull PH	SM	PL	0.04	Holtsmark *et al*. (2009)
Norwegian Red	808 750	Threshold Cross-sectional	SM	SS	0.04	Holtsmark *et al*. (2009)
Norwegian Red	808 750	Threshold Repeatability	SM	SS	0.04	Holtsmark *et al*. (2009)
Norwegian red	808 750	Linear multi-trait	SM	SS	0.02 – 0.03	Holtsmark *et al*. (2009)
Slovak Pinzgau	21 985	Weibull PH	SM	FLPL	0.05	Mészáros *et al*. (2008)
Slovenian Brown	37 908	Weibull PH	SMG	FL	0.094 – 0.099	Jenko *et al*. (2013)
Spanish Holstein-Friesian	21 058	Weibull PH	SMG	FL	0.048 – 0.074	Chirinos *et al*. (2007)
Spanish Holsteins	96 642	STL censored	AM	SNL	0.11	Gonzalez-Recio & Alenda (2007)
South African beef breeds	-	Threshold	SM	FL	0.08	van der Westhuizen *et al*. (2001)
South African Angus	28 671	Threshold	AM	Stayability	0.24 – 0.30	Maiwashe *et al*. (2009)
South African Jersey	181 269	Linear multi-trait	SM	FHL	0.02 – 0.03	Du Toit (2011)
South African Jersey	181 269	Linear multi-trait	AM	FHL	0.01 – 0.03	Du Toit (2011)
South African Holsteins	34 201	Linear bivariate	AM	NL	0.06	Setati *et al*. (2004)
Tunisian Holsteins	36 888	Weibull PH	SM	FL	0.19	M'hamdi *et al*. (2010)

SM=sire model; AM=animal model; SMG=sire maternal grand sire model; PH=proportional hazards; STL=sequential threshold linear; NL=number of lactations initiated; FLPL=functional length of productive life; FHL=functional herd life; FL=functional longevity; LPL=length of productive life; SNL=survival to next lactation; L&T=Linear and threshold; SS=survival scores; Survival to given age;

2.7 Predictors of functional longevity

A number of traits are used to predict longevity in dairy animals. These predictor traits include conformation traits, production traits, somatic cell count, calving traits, cow fertility traits, and milkability. Predictor traits may be included in net merit indices either on their own or in combination with direct longevity as is the case in USA, France and Belgium (Forabosco *et al*., 2009). Recent studies have evaluated dairy form, body capacity, conformation score, rear legs set, hock quality, rump angle and udder traits as early predictors of functional longevity (Zavadilová *et al*., 2011; Zavadilová & Štípková, 2012). The positive correlations between some of these traits and longevity imply longer survival for animals with desirable scores. Although the relationship between functional longevity and some conformation traits appears linear, other traits may have an intermediate optimum and culling risk will increase when type scores deviate from this intermediate optimum (Caraviello *et al*., 2003). Udder traits have been identified as the most important in terms of their contribution to the risk of culling of dairy cows although rump traits, body traits, feet and legs can also be reasons for culling of cows.

2.8 Factors influencing longevity

In proportional hazards modelling, factors influencing the event of interest (e.g time to death) are referred to as covariates and their effects expressed as relative risk of culling. This is the ratio between the estimated risk of being culled under the influence of certain set of environmental covariates [exp (β_i) for level i] and the risk of culling for he reference class (average risk) which is usually set to one ($\beta i=0$) (Sewalem *et al*., 2005b; M'hamdi *et al*., 2010). Risk ratios of greater than one indicate higher culling risk due to that covariate whilst values less than one indicate lower risk and therefore increasing effect of the covariate on functional longevity. For example, a relative culling risk of 2 implies that the animals has twice the risk of being culled than cow in reference class for that covariate whilst a culling risk of 0.5 implies that the animal has a 50% less chance of being culled than cows in reference class. A number of time-dependent covariates have been reported to contribute significantly to the risk of culling and functional longevity. These include relative milk yield, age at first calving, stage of lactation, parity, annual herd changes, herd-year-season, linear type traits and some interactions.

2.8.1 Relative milk yield

Relative milk production is an important covariate because most voluntary culling decisions are based on phenotypic milk yield. High yielding cows are less likely to be culled than their low-yielding herdmates (Passman & Reinhardt, 1999; Sewalem *et al*., 2005b). Conversely, low

producing cows were reported to be at higher relative risk of being culled than their herdmates with above average production (Vukasinovic *et al*., 2001). This was observed in Holstein cattle (Puski *et al*., 2002; Sewalem *et al*., 2005b), Pinzgau cattle (Mészáros *et al*., 2008), Tunisian Holsteins (M'hamdi *et al*., 2010), Kenyan Holstein-Friesian cattle (Ojango *et al*., 2005) and even in buffaloes (Galeazzi *et al*., 2010). Cows with milk production of 1.5 standard deviations below herd mean were reported to be 5.3 times more likely to be culled than cows in reference class (Mészáros *et al*., 2008) whilst from these studies, relative culling risk for cows with low production ranged from 1.25 to 5.3 times that of cows in the reference class. The risk declined significantly with increasing production and became more or less independent of production at very high yields (Galeazzi *et al*., 2010; M'hamdi *et al*., 2010). The high relative risk of culling for low producing cows has been attributed to reproductive problems as well as the animals' susceptibility to teat and hoof problems that increase probability for involuntary culling (Galeazzi *et al*., 2010).

2.8.2 Age at first calving

Functional longevity has been observed to decrease with increasing age at first calving (Nilforooshan & Edriss, 2004; Sewalem *et al*., 2005b; M'hamdi *et al*., 2010; Zavadilová & Štípková, 2013). Heifers calving for the first time at between 24 and 28 months of age tend to have a lower risk of culling than those calving for the first time at a very young or very old age. This risk was severally observed to increase from 0.96 to 1.43 times the risk of the reference class for heifers calving for the first time at 21 and 39 months of age respectively (Sewalem *et al*., 2005b; M'hamdi *et al*., 2010). In the upper limit of this range and where differences between age at first calving classes were small, the risk of culling by age at first calving was reported to remain unchanged until 34 to 37 months (Mészáros *et al*., 2008) beyond which period the risk ratio was observed to be as high as 1.195 times the reference class for cows calving for the first time after 43 months of age. The higher culling risk for heifers with older ages at first calving has been attributed to possible herd management, reproductive and other health problems (Vukasinovic *et al*., 2001; Sewalem *et al*., 2005b) associated with late onset of reproduction in aging cows. Moreover, heifers with delayed calvings are less profitable because of their relatively high rearing costs. High culling risk for heifers calving for the first time at an age of less than 21 months of age has been reported and attributed to possible dystocia (Martinez *et al*., 1983).Although age at first calving had no significant effect on functional longevity, Kenyan Holstein-Friesian cows that calved early for the first time and those that calved late had a higher risk of being culled than cows

in other middle classes clearly demonstrating an intermediate optimum. This was probably due to complications arising from calving difficulties, lower milk production and poor general body condition (Ojango *et al*., 2002).

2.8.3 Stage of lactation and lactation number

Stage of lactation and parity have been reported to individually influence the risk of culling in dairy cattle. Generally, relative risk of culling has been observed to increase along and across lactations (Chrinos *et al*., 2007). Cows towards later stages of lactation were observed to have a probability of culling of 4.06 times higher than a cow of same age at the beginning of her lactation (Ducrocq *et al*., 1988). The high culling risk in later lactations has been attributed to the fact that cows are unlikely to be culled for fertility reasons during the early lactation since most will not be pregnant (Roxstrom & Strandberg, 2002). In contrast, Mészáros *et al*. (2008) and M'hamdi *et al*. (2010) observed high culling risk during the first stage of first lactation. The risk was observed to be four times higher than the risk at later stages of higher parities and was consistent with results from Vukasinovic *et al*. (2001). This was variably attributed to most culling decisions being made during the first half of the first lactation to prevent expenses as well as different selection criteria in first lactating cows.

The risk of culling has also severally been reported to increase with parity (Ducrocq *et al*., 1988; Van der Linde *et al*., 2006; Chirinos *et al*., 2007; Mészáros *et al*., 2008) although some studies have reported decreasing culling risk with parity (e.g. M'hamdi *et al*., 2010). Besides, cows that failed to conceive are usually kept in the herd until the end of lactation. In survival analyses, the contribution of stage of lactation to culling risk is usually considered and classified within parity (e.g. Egger-Danner *et al*., 2005; Bielfeldt *et al*., 2006; Mészáros *et al*., 2008). The most common result for the combined effect of parity × stage of lactation is a decrease of risk during the first, and an increase during further lactations, with a decrease over lactations.

2.8.4 Traits other than production

2.8.4.1 Functional longevity and udder traits

Using linear models and REML, genetic correlation between type traits and functional longevity were reported to range between -0.22 to 0.05 for udder traits and average 0.27 for capacity, 0.14 for feet and legs, -0.20 for conformation and -0.26 for dairy form in Czech Holsteins (Zavadilová & Štípková, 2012). Slightly higher estimates ranging between 0.36 and 0.5 were reported by

Rodgers *et al*. (1999) and Tsurunta *et al*. (2005) for genetic correlation between type traits and functional longevity. Earlier studies in Dutch Friesian cattle found higher correlations between subjective score for udder traits and longevity of between 0.77 and 0.93 which were attributed to probable upgrading of the Friesian breed by the Holstein (Vollema & Groen, 1997). In South African Holstein cattle, Setati *et al*. (2004) reported correlations of between -0.15 and 0.48 between conformation/type traits and longevity. Such correlations are relatively high and could probably be due to low emphasis on selection against poor type traits or durability at time of study. Although linear models and REML have widely been used to estimate correlation between type traits and longevity, they have their own limitations since the joint distributions are difficult to describe using the common methods, if not impossible (Gonzalez-Recio & Alenda, 2007). Damgaard & Korsgaard (2006) presented a Gibbs sampler for joint Bayesian analysis as an appropriate method for estimating correlation between a threshold character and a survival trait. This was however observed to be demanding in terms of computing capacity. Gonzalez-Recio & Alenda (2007) proposed a bivariate sequential threshold model for joint analysis of one discrete-time survival trait and one Gaussian trait.

2.8.4.2 Udder traits and survival analysis

Survival analysis provides an ideal tool for checking the existence of correlation between longevity and type traits through determination of the contribution of identified type traits to the risk of culling and therefore longevity. Type traits with the greatest influence on the risk of culling in dairy cattle have been reported to be those linked to udder traits (Larroque & Ducrocq, 2001; Schneider *et al*., 2003; Setati *et al*., 2004; Bouška *et al*., 2006; Zavadilová *et al*., 2009). Udder type traits contribute to culling and, hence, affect longevity, probably through their influence on mastitis and other disease incidence. Cows with good udders are more likely to avoid involuntary culling than those with poor udders. The relative contribution of udder type traits to risk of culling and hence probability of survival has been well documented (e.g. Bünger *et al*., 2001; Dadpasand *et al*. 2008; Zavadilová *et al*., 2011). Some researchers have listed udder traits with significant impact on longevity in their order of importance as udder depth, fore udder attachment, front teat placement, udder support, udder cleft and teat length (Boettcher *et al*., 1999; Bünger & Swalve, 1999; Caraviello *et al*., 2003). Dadpasand *et al*. (2008) observed a slightly different order consisting of fore udder attachment, udder depth, fore teat placement and for suspensory ligament. Udder depth has been reported to have the highest relative contribution to survival and therefore the highest effect on cow survival after correction for milk production (Bünger & Swalve, 1999;

Caraviello *et al*., 2003; Zavadilová *et al*., 2011). Dadpasand *et al*. (2008), Sewalam *et al*. (2005a) and Caraviello *et al*. (2003 & 2004b) reported an intermediate optimum for udder depth implying that cows with very deep or very shallow udders were at high risk of being culled from the herds. Among US Jersey cows, udder depth scores of between 6 and 10 on a scale of 1 to 100 had 1.6 times more relative risk of involuntary culling than cows with scores between 21 and 25 whilst cows with udder depth scores of 41 to 45 had a relative risk of 0.7 times that of cows with scores of 21 to 25 (Caraviello *et al*., 2003). In the same study, cows with udder support scores of 6 to 10 on a scale of 1 to 100 were found to have relative risk of culling of nearly 1.8 times that of cows with intermediate scores, especially at the lower end of the scale. The importance of fore-udder attachment and the central ligament has also been observed with the latter reported to contribute more to the relative risk of culling than rear-udder height and rear-udder attachment (Sewalem *et al*., 2004; Schneider *et al*., 2005). Regardless of the order of importance, Larroque and Ducrocq (2001) pointed out that traits related to udder support, particularly udder depth and central ligament attachment, better explained culling differences than teat length and teat placement.

In Croatian Simmental cattle, cows that scored lower for suspensory ligament attachment, rear udder length and teat thickness had approximately 1.5 to 2.0 times higher risk of being culled than those with scores of at least four (Jovanovac & Raguž, 2011). This concurred with results from Zavadilová *et al*. (2011). Teat placement has also been reported to influence culling and, therefore, longevity in dairy cattle. Cows with extremely closely placed rear teats are more likely candidates for culling than those with extremely wide rear teats (Ducrocq, 2002; Schneider *et al*., 2003; Sewalem *et al*., 2005b) as they present problems of teat-cup placement resulting in delays in the milking process especially in large herds. By contrast, Zavadilová *et al*. (2011) reported small contribution of teat placement to survival and hence functional longevity.

Traits other than production that have been reported to have a significant effect on functional longevity have been identified as mainly as the composite conformation and udder overall traits (Berry *et al*., 2005). These traits have traditionally been used as early predictors of functional longevity in dairy cattle on the basis of the positive and generally low to intermediate genetic correlation between some of them and functional longevity (Bünger & Swalve, 1999; Jovanovac & Raguz, 2011). This has its advantages. Measured earlier in life, cows with predicted poor functional longevity as indicated by defective type and conformation traits can be removed from herds earlier without waiting for a large percentage of their female progeny to be culled (Weigel *et al*., 1998). This saves on rearing costs for animals that would otherwise be culled later in life.

Furthermore, heritability estimates for some type traits have been reported to be higher (e.g. Zavadilová & Štípková, 2012) than for directly measured functional longevity. This is linked to an improvement in the estimation of breeding values for those type and conformation traits with positive influence of longevity.

2.8.5 Annual change in herd size

Of all the time dependent effects influencing the culling risk, annual change in herd size has the least impact on the change in the log likelihood compared to the other main effects (Sewalem *et al*., 2005b). Shrinking herds have been reported to have relatively higher culling risks than herds with stable or increasing herd sizes in Slovak Pinzgau, Canadian Holstein, Jersey and Tunisian Holsteins (Sewalem *et al*., 2005b; Mészáros *et al*., 2008; M'hamdi *et al*., 2010). Herd size had 1.12 times risk of culling in shrinking herds than in the stable herds. The risk of culling in Tunisian Holsteins was observed to decrease in herds increasing annually in size by between 5 and 15% and those herds increasing annually by more than 25% when compared to stable herds (M'hamdi *et al*., 2010).

2.9 Conclusion

The relatively high economic importance of functional longevity justifies the need to genetically evaluate the trait making it an ideal trait for incorporation into the overall breeding objective for dairy cattle in those countries yet to adopt this. Different models for evaluation of longevity have been discussed and the advantages and disadvantages of each outlined. Various comparative studies have indicated that PH modeling of survival is more efficient than linear, random regression and threshold modeling of functional longevity. This is because PH models appropriately handle time dependence and censoring in a relatively more robust way than random regression and threshold models. Linear modeling cannot even handle these two phenomena, leading to possible loss of information from the analyses. Moreover, proportional hazards models have been reported to produce relatively higher heritability estimates for longevity than linear, random regression and threshold models implying more rapid genetic progress when the trait is evaluated with PH models. Countries can however use any of the models depending on the available resources, available data and technical capabilities. However, it is difficult to come up with an internationally accepted method of ranking sires for functional longevity primarily because different countries use different definitions for the trait longevity. Sire ranking can therefore be improved through development of models that optimally utilise all the available information to accurately derive and apply genetic parameters estimated in genetic evaluation of animals. This

remains a challenge for developing countries mainly in sub-Saharan Africa where milk recording schemes are yet to be fully developed. South Africa has an advantage in that it already has a relatively comprehensive functional milk recording scheme. The appropriate methodologies and software are also readily available for proportional hazards modeling. Opportunities therefore exist for incorporation of the trait in the breeding objective for South African Holsteins as part of the wider balanced breeding concept which currently incorporates production traits, somatic cell counts and calving interval.

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Chapter 3

Non-genetic factors influencing functional longevity of South African Holstein cows

3.1 Abstract

Fixed effects that contribute to the risk of culling for dairy cattle and therefore influence functional longevity of South African Holsteins were determined using a piecewise Weibull proportional hazards model. Data comprised of production records of 161 222 daughters of 2 015 sires, for the period 1995 to 2013. Data were analysed with Survival Kit version 6. The model included the fixed time-independent effect of age at first calving, fixed time-dependent effect of region by year of calving, number of lactations by within-herd milk production class, within-herd protein and fat percent production classes by year of calving and the combined time-dependent effect of herd size by annual herd size change. A cox model was used to estimate the survival and hazards functions. All fitted effects had a significant effect ($P<0.05$) on the relative risk of culling. Cows in all regions were at a lower risk of being culled recently than they were in 1995. For cows that calved for the first time in 2002, survival function was best in Northern Cape, Western Cape and the Free State Provinces whilst it was worst in the Eastern Cape, Kwa-Zulu Natal and the combined Gauteng and North Western Provinces. Within-herd milk production had the largest contribution to the risk of culling whilst region x year and within-herd protein production percent were second and third most important factors respectively. For all lactations, risk of culling was highest for second stage of lactation (271- 380 days) and lowest during first stage of lactation (1-270 days) for all lactations. High milk producing cows resisted voluntary culling more than poor yielding cows. Animals in the Eastern Cape were more predisposed to culling than those from other regions. Cows were at a higher risk of being culled for low within-herd protein production percent than within-herd fat production percent. Heifers calving at an older age (37 – 42 months of age) had a higher risk of being culled than young heifers. Animals with multiple lactations were at higher risk of being culled than those with a single lactation. The higher relative risk of culling for cows with multiple lactations indicated the tendency of dairy farmers to retain younger cows in herds than older cows. Cows in shrinking medium and large herds were at a higher risk of being culled and therefore most likely to have compromised functional longevity than those in expanding herds.

Keywords: Weibull, fixed covariates, relative risk, culling

3.2 Introduction

South African Holstein cattle are routinely evaluated for production, calving interval and somatic cell count. The results from the genetic evaluation are then combined with economic weights for the traits to produce a Holstein Profit Ranking index which reflects the net merit of the animals in monetary form, an important indicator of the economic viability of the animal. Notwithstanding a good net merit for production and fitness, an animal can only be profitable within the herd for as long as it can sustain its productivity over a reasonably long period of time. Within this context, functional longevity, which measures the cow ability to resist both voluntary culling and involuntary culling, becomes as important a trait as production and other fitness traits to justify its inclusion in the breeding objective for dairy cattle. Voluntary culling is mainly for low production and involuntary culling is done for reasons other than production The few studies carried out to date on longevity among South African Holsteins have shown a decrease in phenotypic trends for longevity as measured by the proportion of cows completing lactations (Banga *et al*., 2002). This could be attributed to a number of factors including the lack of genetic selection for the trait and a number of non-genetic factors with a significant contribution to the risk of cows being culled from herds.

Besides the animal's innate ability to prolong survival, non-genetic factors contribute significantly to functional longevity (Ojango *et al*., 2005; Terawaki & Ducrocq, 2009; du Toit, 2011). The main factors are phenotypic measures of production traits, age at first calving, lactation number, geographical region, as well as age of the animals. Most culling decisions are based on the phenotypic measurement of production. High yielding cows are less likely to be culled than their low-yielding herdmates (Passman & Reinhardt, 1999; Sewalem *et al*., 2005). Conversely, low producing cows are at a higher risk of being culled than their herdmates with above average production (Vukasinovic *et al*., 2001). This has been observed in several dairy cattle populations (Sewalem *et al*., 2005; Mészáros *et al*., 2008; M'hamdi *et al*., 2010; Ojango *et al*., 2005). The risk of culling due to production declines with increasing production and becomes more or less independent of production at very high yields (Galeazzi *et al*., 2010; M'hamdi *et al*., 2010). In most countries, including South Africa, dairy farmers are also being paid for milk deliveries on the basis of protein and butterfat percentage content of milk beside the total milk volume, somatic cell count and microbiological quality. This has resulted in cows being culled for poor butterfat and protein percentage production as well.

Relative risk of culling increases with the age at first calving (Ducrocq, 2005). This implies that functional longevity declines with increasing age at first calving (Nilforooshan & Edriss, 2004; Sewalem *et al*., 2005; M'hamdi *et al*., 2010; Zavadilová & Štípková, 2013). This could be attributed to reproductive and other health problems associated with very late onset of reproduction in aging heifers (Vukasinovic *et al*., 2001; Sewalem *et al*., 2005). Heifers calving at less than 20 months of age also have a relatively higher risk of being culled than those calving at more than 22 months of age. This could be attributed to possible dystocia with early onset of reproduction (Martinez *et al*., 1983), poor herd management or general poor condition of the heifers. Inconsistencies in the effect of age at first calving on longevity have been observed though. Age at first calving has, in other studies, been reported to have no significant influence on functional longevity (Ducrocq, 1994; Ojango *et al*., 2005; Jenko *et al*., 2013) and this was probably due to to differences in target age at first calving between different herd management systems (Bielfeldt *et al*., 2006).

Other factors contributing the probability of culling among dairy cattle have been identified as the combined effect of stage of lactation and lactation number, annual change in herd size and year of calving. Lactation number individually influence the risk of culling in dairy cattle. Relative risk of culling has been observed to increase along and across lactations (Chirinos *et al*., 2007). Cows in higher lactations are more predisposed to culling than those in lower lactations (Ducrocq *et al*., 1988; Van der Linde *et al*., 2006; Chirinos *et al*., 2007; Mészáros *et al*., 2008) although some studies have reported decreasing culling risk with lactation number (e.g. M'hamdi *et al*., 2010). Farmers tend to retain cows in lower lactations than those in higher lactations. Within lactation, cows are more likely to be culled towards the end of the lactation than at the beginning (Ducrocq *et al*., 1988). This is probably because farmers are unlikely to cull cows for fertility reasons during the early lactation since most will not be pregnant (Roxstrom & Strandberg, 2002). Besides, cows that fail to conceive are usually kept in the herd until the end of lactation to optimise returns through sustained milk production. Because of this, the contribution of stage of lactation to culling risk is usually considered and classified within lactation (e.g. Egger-Danner *et al*., 2005; Bielfeldt *et al*., 2006; Mészáros *et al*., 2008). The most common result for the combined effect of stage of lactation x parity is a decrease of risk during the first, and an increase during further lactations, with an overall decrease across lactations.

Previous studies have analysed longevity for South African dairy cattle (Setati *et al*., 2004; du Toit, 2011) with linear bivariate and multivariate sire and animal models. Despite the shortcomings

associated with linear models for evaluation of longevity, the studies collectively identified herd-year, age at first calving, season of calving, registry status, protein yield and fat yield as important determinants of binary longevity. The current study used a different modeling approach but with basically the same fixed non-genetic effects and their combinations. A revised proportional hazards model as proposed by Ducrocq (2005) which was different from previous models was used. It simultaneously modeled hazard within and across lactation. The model is more flexible with a piecewise Weibull baseline defined within and across lactations. Furthermore, the definition of the stage of lactation in the new model was objectively based on stages during the lactation when slope of the hazard curve changed drastically. This was an improvement on the previous model in which the stage of lactation was defined arbitrarily (Ducrocq, 1999). Generally, the model used in this study could better account for changes in effects of non-genetic effects with time as was demonstrated by the changes in the Weibull shape parameter (ρ) with time. The obtained relative risk ratios in this study were therefore better indicators of the contribution of the covariates to the risk of culling. The effect of various covariates on the functional longevity of South African Holstein cattle has not been quantified with a proportional hazards model to establish those covariates contributing the most to the risk of culling. This study was carried out to determine the fixed effects that influence longevity in South African Holstein cattle.

3.3 Materials and methods

A total of 3 492 077 lactation records and 283 849 type and conformation records for Holstein cows born between 1951 and 2002, collected under the National Milk Recording and Improvement Scheme, were obtained from the Integrated Registration and Genetic Information System (INTERGIS). These included records from the Eastern Cape (EC), Western Cape (WC), North Western Province (NW), Kwa Zulu Natal (KZN), Free State (FS) and the combined Gauteng-North Western Provinces. Variables in the data sets were as shown in APPENDIX 1. Data were systematically processed through editing and preparation with SAS Version 9.3 (SAS, 2002-2010) and FORTRAN 90. Data were analysed with Survival kit v6 (Ducrocq *et al*., 2012).

3.3.1 Data edits and preparation

3.3.1.1 Data edits

Initial edits were carried out with Statistical Analysis System (SAS) Version 9.3 (SAS, 2002-2010). These removed records of cows with unknown or missing date of birth, date of first calving, herd code, pedigree, milk, butterfat and protein yield. Only cows with first five calvings between 1 January 1988 and 30 April 2013 were included in the analyses. Initially, all cows that calved for

the first time at less than 18 months and more than 50 months of age were deleted. Later, analysis was restricted to cows with first calving at 20 to 42 months of age. Table 3.1 shows the initial editing criteria, number and percentage of data lost during editing.

Table 3.1 Proportion of data lost after initial edits

Editing criteria	Records lost	% lost	Cumulative loss (%)
Unknown yield, birth date and herd code	517 226	14.81	14.81
Unknown date of first calving	509 468	17.13	29.40
18 months > age at first calving > 50 months	122 038	4.95	32.90
Lactations > 17 and outside calving age class within lactation	11 447	0.49	33.23

3.3.1.2 Generation of variables

Further edits and generation (calculation) of new variables were done using FORTRAN 90. Year of calving was restricted to the period 1995 to 2013 for years of cow birth stretching from 1985 to 2002. Cows with less than five lactations that were started before 1988 were excluded from the analysis. The variables: age at first calving in months, survival (days) from first calving to last date of lifetime production, lactation length, calving interval, herd-year-season, year-season, herd size per trimester and annual herd size change measured at beginning of first trimester (January) of every year were computed. Lactation end date, whether censored or not, was determined just as was date of exit of cow from herd and date of birth of dam.

3.3.2 Data classification

Three stages of lactation classes and a dry period were created (1 – 270 days; 271 – 380 days; 381 – 800 days and the dry period). In the absence of adjustment factors for South African Holsteins, actual production (milk, butterfat and protein) yield were adjusted to standard 305-day lactation yield using the Holstein cattle indices for French Holstein population. Ten relative milk yield classes calculated as the number of standard deviations of milk yield from the herd mean were created whilst five relative butterfat and relative milk protein classes were also created as indicated in Tables 3.3 and 3.4. Variations in all the production traits were expressed within-herd. The production standard deviations were computed as follows: -

$$relative\ milk\ yield(rmy) = \frac{within\ herd\ milk\ yield - herd\ mean}{k\ x\ sd} \quad (1)$$

where k was a multiplicative factor (in this study, k=0.75) meant to reduce standard errors and ensure an even distribution of number of records per class and sd was standard deviation for milk. The same formula was used to compute standard deviation units for butterfat and protein percentage production.

Table 3.2 Lower and upper limits of class of relative milk yield in standard deviation units

Class	Lower limit	Upper limit
1		-1.281
2	-1.281	-0.843
3	-0.843	-0.524
4	-0.524	-0.255
5	-0.255	0
6	0	0.255
7	0.255	0.524
8	0.524	0.843
9	0.843	1.281
10	1.281	

Table 3.3 Lower and upper limits of class of relative butterfat and milk protein in standard deviation units

Class	Relative BFC/Protein yield SD units	
	Lower limit	Upper limit
1		-0.843
2	-0.843	-0.255
3	-0.255	0.255
4	0.255	0.843
5	0.843	

Annual herd size variation was incorporated in the model as an interaction between herd size and annual herd size variation. A total of 9 classes and sub-classes were created as shown in Table 3.4.

Table 3.4 Annual herd size change by herd size classes and sub-classes

Number of cows (Herd size: Class)	Sub-class	Herd size change (%)	
		Lower bound	Upper bounds
< 5	1	0	0
5 – 19	2		- 10
	3	-10	15
	4	>15	
20 – 49	5		-10
and	6	-10	-5
> 50	7	-5	5
	8	5	15
	9		>15

3.3.3 Data censoring

Complete records were uncensored whilst the incomplete records were right censored. All cows observed to be alive at the time of data acquisition and those removed from the herds deliberately through decision of the farmers were right censored from the date of the end of the last known lactation. This was because their survival was assumed to be longer than observed. Cows in lactations beyond the fifth were censored at end of the fifth lactation. Cows with lactations greater than 800 days were censored at that day count to avoid favouring these animals during analysis. Censored records also included those of animals that were alive at limit date, records of cows in disappearing herds, records of cows with lactations started after limit date and records of cows with missing lactations. Records of cows known to have either died (with date of death) or culled for various reasons were considered correct and therefore uncensored.

The date of end of lactation was assumed to be the date of culling. Full termination codes defining the reasons for exit from herds included death, culling for low production, infertility, poor conformation traits (udder, feet and legs), mastitis, injury and clinical reasons are in Appendix 7.3. These were classified into four classes: Normal lactation, Sold, Died and other causes of termination. Table 3.5 shows the total number of animals (not records) that were excluded from analyses for various reasons.

Table 3.5 Excluded records after FORTRAN 90

Reasons for deletion/exclusion	Numbers
Cows with unknown sires	88 872
Cows with first lactation after limit date	554
Cows with lactation length=0 for first lactation	42
Cows with unknown date of birth	1
Other	9

3.3.4 Data analyses

Edited data were analysed using a proportional hazards model with a fixed effects model using the FORTRAN based software Survival Kit Version 6 (Ducrocq *et al*., 2012). Initially, the Kaplan-Meir survival and the hazard functions were estimated by region and herd status using a non-parametric Cox regression equation (Kaplan & Meir, 1958).

A model assuming a piecewise Weibull distribution of the baseline hazard function was used in this study. It allowed stronger inferences about the survival times to be made because the model defined the baseline hazard function as a piecewise Weibull hazard function with shape parameter ρ differing for each combination of lactation and stage of lactation (Ducrocq, 2005). Evidence has indicated that the baseline hazard function assumes different slopes for each of the lactations although they have the same shape. Describing the variation of the hazard within and across parities removes the need to incorporate the combined stage of lactation by parity in the piecewise Weibull model. With five lactations and four stages of lactation, this gave a total of 20 Weibull parameters each one representing a time (stage of lactation x lactation number) combination. The lactation stages were defined according to τ, the number of days since the most recent calving, with change at time 0, 270, 380 and the dry period for each lactation. These were validated though a plot of the empirical within lactation estimate of the hazard function (Kalbfleisch & Prentice, 1980) derived from the within lactation survival curves (Figure 3.1). The output from the model relates directly to duration of survival and as such, inferences can be made about the true event. The following fixed effects proportional hazards model was used: -

$$\lambda_{ijklmnop}(t) = \lambda_0(t) \exp(yr_i + ym_j + sm_k + age_l + pcy_m + fcy_n + hc_o) \quad (2)$$

where $\lambda_{ijklmn}(t)$ is the hazard function of the cow (daughter ***k*** of sire ***n***) with recorded herd life of ***t*** (days from first calving to culling or censoring), $\lambda_0(t)$ is the piecewise Weibull baseline hazard function for the n^{th} period (stage of lactation 1 to 4) of the r^{th} parity (1 – 5) beginning in 1988 to 2013 with scale parameter λ and shape parameter ρ. This resulted in 19 baseline hazard functions. All the other effects were as described in Table 3.6. The statistical significance of each of the fixed effects was determined using the likelihood ratio tests with a fixed effects model. The magnitude of the change in the negative log likelihood values between a full model and a reduced model (without each of the fixed effects) gave an indication of the relative importance of each effect.

Table 3.6 Description of effects included in the Weibull model

Effect	Description
yr_i	fixed time-dependent effect of ith region (6 regions) x year of calving (19 years: 1995 to 2013)
ym_j	fixed time-dependent effect of jth within-herd milk production class x year-season with years of 1995 to 2013 with 4 seasons and 10 milk classes
age_k	fixed time- independent effect of the kth age at first calving classed by one-month interval from 20 to 42 months of age
sm_l	fixed time-dependent effect of number of lactations x stage of lactation x within-herd milk production class (single=1 and multiple lactation=2+, four stages of lactation and 10 milk classes);
py_m	Fixed time dependent effect of protein percent production class (5 classes) x year of calving (1995 – 2013);
fy_n	Combined fixed time dependent effect of fat percent production class (5 classes) x year of calving (1995 – 2013);
hc_o	Combined fixed time dependent effect of herd size x annual herd size change classed as herds with less than 5 cows, 5 to 19 cows with three sub-classes of herd size variation (decrease by 10%, stable size, increase by more than 10 %), 20 to 49 cows and more than 50 cows with five sub-classes (decrease by 10%, decrease by 5 to 10%, stable herds, increase by 5 to 10% and increase by more than 10%)

3.4 Results

Table 3.7 shows the structure of the retained records that were used in the Weibull proportional hazards modelling using Survival kit. About 41% of the records were censored with a slightly

higher average failure time from calving for uncensored than censored records. There were 728 animals with lactation greater than 800 days whose mean length was 951 days.

Table 3.7 Structure of the retained records used in Weibull analysis

Description		Numbers
Total number of elementary records*		2 299 706
Cows included in analysis		161 222
Cows with reconstructed year of birth		161 222
Cows with known maternal grand sire		76 252
Cows still alive at analysis		1 118
Cows still lactating		1 106
Cows with censored records		47 370
Censored dried cows (forced)		47
Censored records		65 227
		(40.48%)
Uncensored records		95 995
		(59.52%)
Censored dry cows (forced)		47
Average within-lactation failure or censoring time (d)	*Censored records:*	258
	Uncensored records:	261
Maximum lactation length for uncensored records (d)		951

*Individual records for each period of change as per the triplets

3.4.1 Length of productive life by year

Functional longevity is declining among Holstein cattle in South Africa. Cows that calved for the first time in 2000 had relatively longer length of productive life than those that delivered a calf for the first time in 2004 and 2008. Animals that first calved in 2008 had the shortest length of productive life. The length of productive life for cows that first calved in 2000, 2004 and 2008 are shown in Table 3.8. Trends in the survival function for these cows are shown in Figure 3.2.

Table 3.8 Average length of productive life (LPL) for cows calving for the first time in 2000, 2004 and 2008

Year	Record status	Number of records	Average LPL (days)	Maximum LPL	Proportion censored (%)
2000	Censored	4 115	894	2645	46.24
	Uncensored	4 784	830	2894	
2004	Censored	4 408	885	2705	36.92
	Uncensored	7 531	818	2833	
2008	Censored	2 645	730	2173	39.08
	Uncensored	4 124	682	2151	

3.4.2 Hazard and Survivor curves

The empirical within lactation hazard function for the first three lactations plotted from the Kaplan-Meir estimates of the survival function for cows that calved for the first time in 2002 are illustrated in Figure 3.1. The year 2002 was chosen because of the relatively high number of records of cows calving for the first time during that period. Evidently, hazard differed within and across lactations. Hazard increased until about 270 to 305 days peaking at a period coinciding with the time most cows are dried off and poor producers culled off. Thereafter, with a few animals with long lactations still in herds, hazard fluctuated through the days from calving but showing a steady increase. The trend of the hazard functions in all lactations justifies the need to use a piecewise Weibull model with the baseline hazard changing at 270 and 380 days from calving as was done in this study.

The survival function for the cows in the different regions is shown in Figure 3.2. Two clusters were evident. Cows in Gauteng/North Western, Eastern Cape and KwaZulu Natal provinces showed a steeper decrease in survival than those in Northern Cape, Free State and Western Cape provinces. Survival was worst for Eastern Cape and best for cows in Northern Cape.

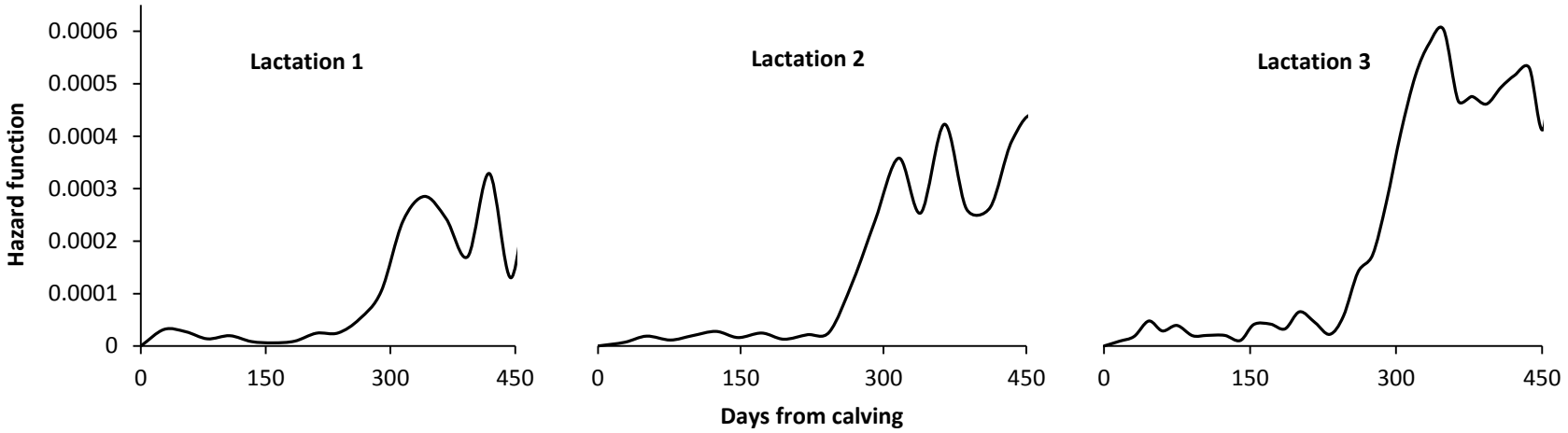

Figure 3.1. Within lactation estimate of the empirical hazard function for the first three lactations derived from the Kaplan–Meier estimates for cows calving for the first time in 2002.

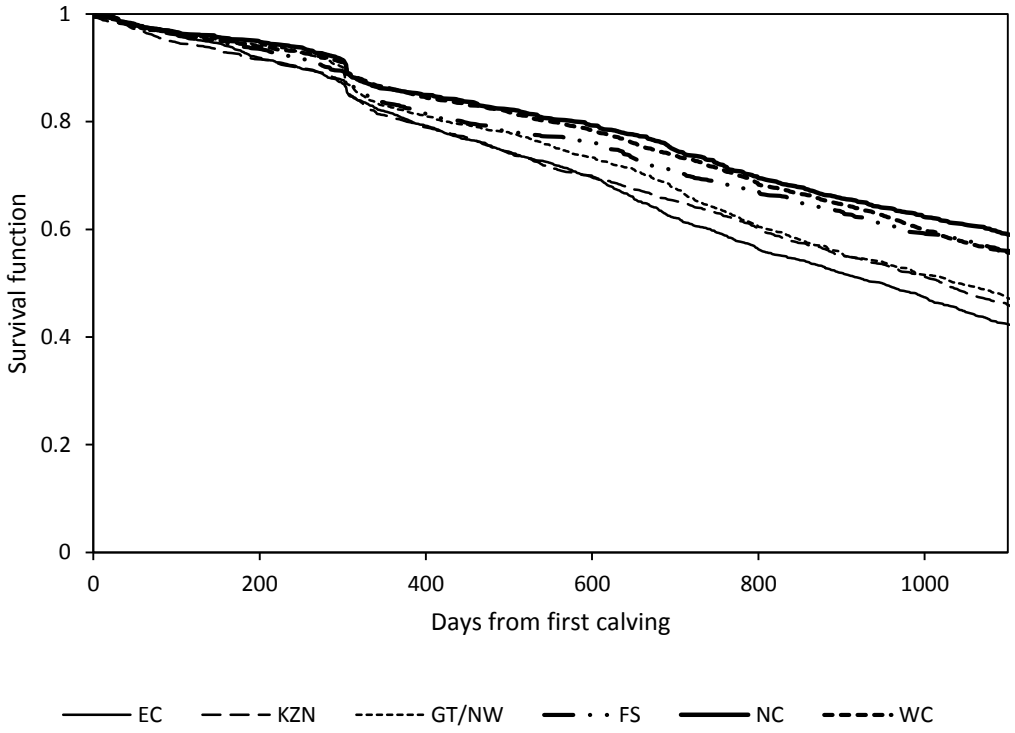

Figure 3.2 Survival function for cows calving for the first time in 2002 in Western Cape (WC), Eastern Cape (EC), Gauteng/North Western (G/NW), Free State (FS), Northern Cape (NC) and KwaZulu Natal Provinces for the first three years of life (1100 days)

Figure 3.3 shows comparison of survival for cows calving for the first time in 2000, 2004 and 2008. Evidently, cows that calved for the first time in 2000 had better survival than those calving in 2004 and 2008. This implied decreasing survival and functional longevity over the years.

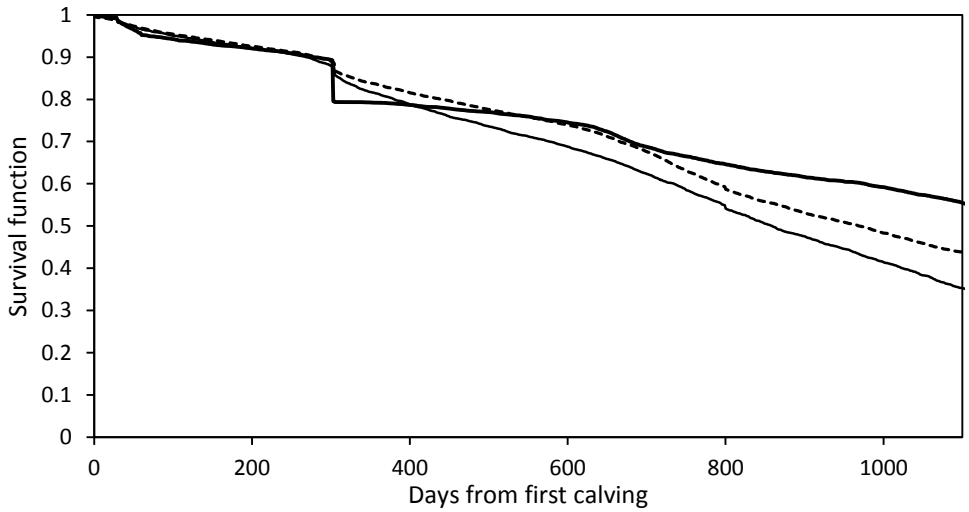

Figure 3.3 Raw survivor curves of daughters calving for the first time in 2008 (bottom line), 2004 (middle line) and 2000 (top line) during the first three years of life.

3.4.3 Weibull parameters

The magnitude of the value of the Weibull shape parameter (ρ) for any covariate indicates trend in risk. Values of ρ (rho) less than 1 indicate that risk is decreasing whilst values of ρ above 1 indicate increasing risk. A value of 1 indicates a constant risk. The larger the ρ value is, the faster the increase in relative risk over time. Figure 3.4 shows the values of the Weibull shape parameter for stage of lactation x lactation. The variability of the Weibull parameter values clearly indicate that hazard functions vary across the different stages of lactation within a lactation. As such, the hazard cannot be treated as a constant function for the entire lactation let alone herd life further justifying the use of a piecewise Weibull model in survival analysis. The value of ρ was markedly lower (0.92 to 1.07) for the first stage (0 – 270 days) of all lactations indicating a low predisposition to culling for animals in early lactation. Relative risk increased tremendously after the first stage of lactation as farmers probably try to manage costs by early culling poor producers to limit feeding expenditure on young non-performing cows which still have high demands for the expensive protein in diets for both growth and production. The consistently high risk of culling for the period 270 to 380 days (RR=3.26 to 4.27) for all parities is not unexpected since most farmers tend to cull their cows on yield at the end of lactation which normally is after 305 days, which falls within this period. The probability of culling for the third stage of lactation (RR=2.74 to 3.09) was significantly lower than for the second stage of lactation (RR=3.26 to 4.27) stage. Within lactation comparisons show a significant increase in relative risk during the second and third stages of all lactations.

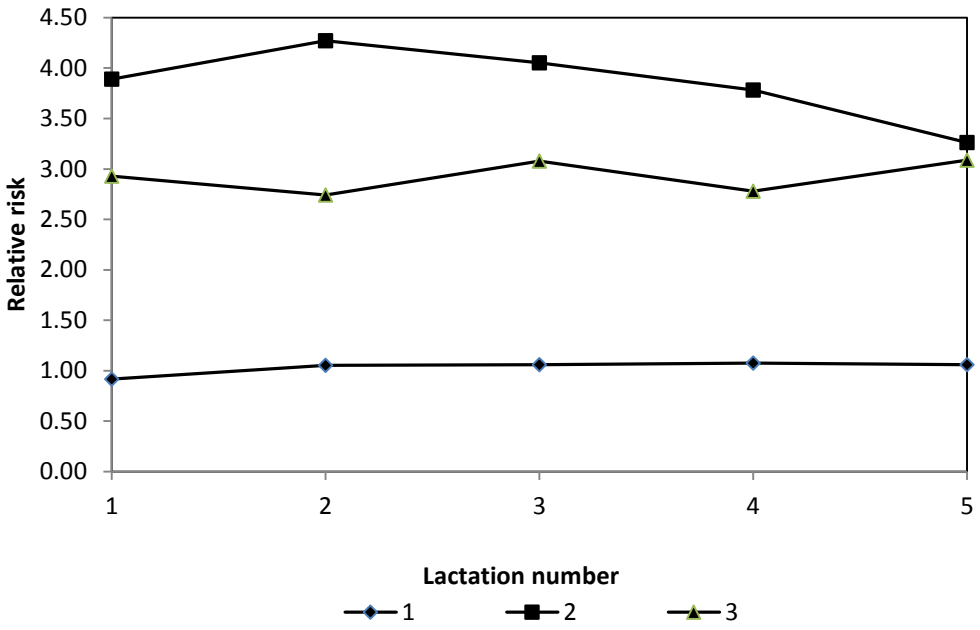

Figure 3.4 Estimates of the Weibull shape parameter (ρ) for the three stages of lactation (stage 1 = 1 to 270 days in milk; stage 2=270 to 380 days in milk; stage 3=days in milk >380 days) by true lactation.

The period after the third stage of lactation was the dry period after which animals are expected to calve down for the next lactation period. As such, the relative risk of culling for the cows for production related reasons will be assumed to be zero and was set at 1 (reference point) in this analysis to avoid giving extra credit to cows with a long dry period.

3.4.4 Effects of systematic environmental factors on longevity

The results of the log likelihood ratio test are shown in Table 3.9. All covariates fitted in the fixed effects model significantly contributed to the risk of culling in South African Holsteins ($P<0.0001$) and therefore functional longevity. The magnitude of the change in the -2 log likelihood identified the region x year, within-herd milk production class and within-herd protein production percent as covariates with the largest influence on the hazard function. The number of lactations x within-herd milk yield, though significant, had the least influence on risk of culling. Age at first calving also significantly ($P<0.0001$) contributed to the risk of culling for the cows.

Table 3.9 Results of the likelihood ratio tests (-2Log Likelihood full model=1 411 876.081)

Effect	-2 LL excluding effect	-2ΔLL	DF	P-value	R^2 of MADDALA
Age at first calving	1 412 945.115	1 069.00	22	P <0.0001	0.2085
Region by year of calving	1 417 243.122	5 367.10	119	P <0.0001	0.1872
Within-herd milk yield class by year-season	1 422 788.174	10 912.00	759	P <0.0001	0.1586
Number of lactations by within-herd milk yield class	1 412 010.442	134.33	19	P <0.0001	0.2130
Within-herd fat percent class by year of calving	1 413 648.092	1 772.00	94	P <0.0001	0.2051
Within-herd protein percent class by year of calving	1 414 223.924	2 347.80	94	P <0.0001	0.2023
Herd size by annual herd size change	1 413 763.450	1 887.40	13	P <0.0001	0.2044

*Obtained by fitting a fixed effects model without random effects

3.4.4.1 Effect of age at first calving

Age at calving contributed significantly (P<0.05) to the risk of culling. Heifers calving at very old age, 42 months, were 1.926 times at risk of being culled than the average heifers (class=24) whilst those calving at a very young age, 20 months, were 1.007 times more likely to be culled than the average cows. Heifers calving at 22 to 23 months of age had the least risk of being culled (RR=0.957) when compared with the average heifers. The highest jump in risk was observed at 40 (RR=1.342) to 41 (RR=1.926) months of age prior to which estimated relative risk was increasing gradually. Figure 3.5 shows the effect of age at calving on relative risk of culling of heifers. Heifers coming into production late in life could probably be constrained by fertility problems and as such farmers tended to cull these animals early from the herds thereby increasing their risk of being removed from herds. The marginally higher culling risk associated with the very young heifers could be due to problems relating to dystocia and associated problems common among young growing heifers.

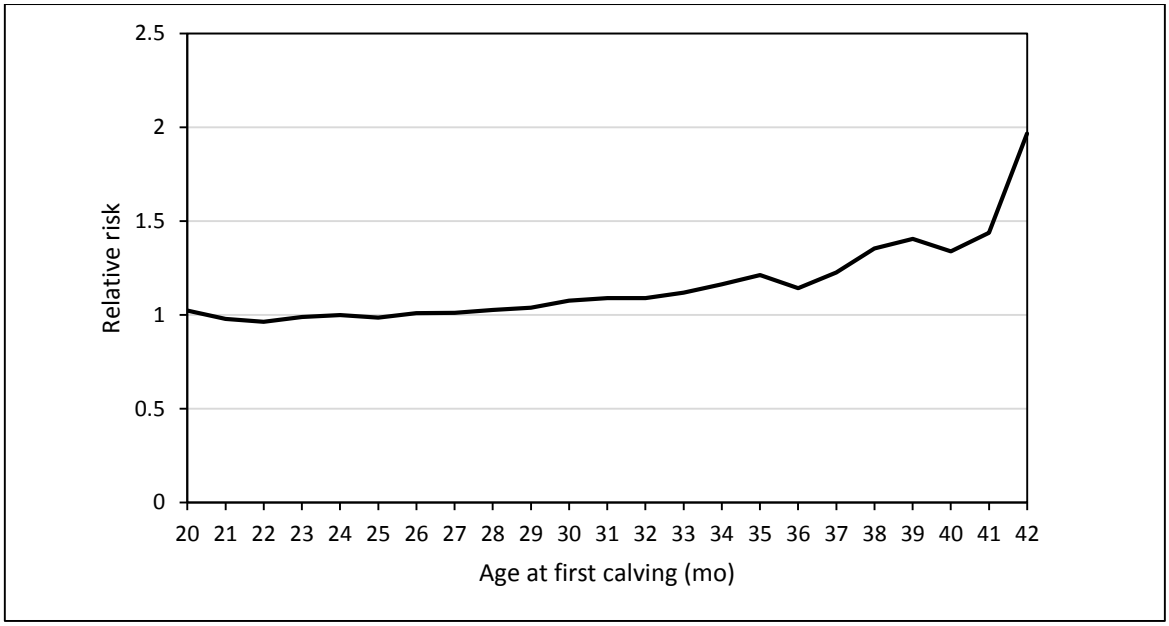

Figure 3.5 Effect of age at first calving on relative risk

3.4.4.2 Region by year of calving

The region by year combination was included in the model to account for any systematic differences in the culling policies of dairy farmers in different regions of South Africa due to variations in climate, systems of production and marketing. The location of the herds and the animals contributed to risk of their culling. Region x year was the second most important effect, after milk yield, contributing to the risk of culling. Generally, cows in all regions were at a lower risk of being culled post-2000 than they were before this period (Figure 3.6). There was a small but gradual decline in risk of culling across all the regions with time from 2003 to 2013. The biggest decrease in risk was during the period 1996/1997. Table 3.10 shows the average length of productive life (days) per region for censored and uncensored data for cows that calved for the first time in 2000. Cows in Eastern Cape, combined Gauteng and North Western and the Free State Province showed a consistently higher predisposition to culling than animals in the Northern Cape, Western Cape and Kwa Zulu Natal (Figure 3.6). Cows in Kwa Zulu Natal were, on average, 1.86 times at risk of being culled than those in the Eastern Cape (reference class) whilst cows in the Free State were 1.43 times the risk of being culled than the average cows. The combined effect of year of calving and region on the risk of culling is shown in Figure 3.6.

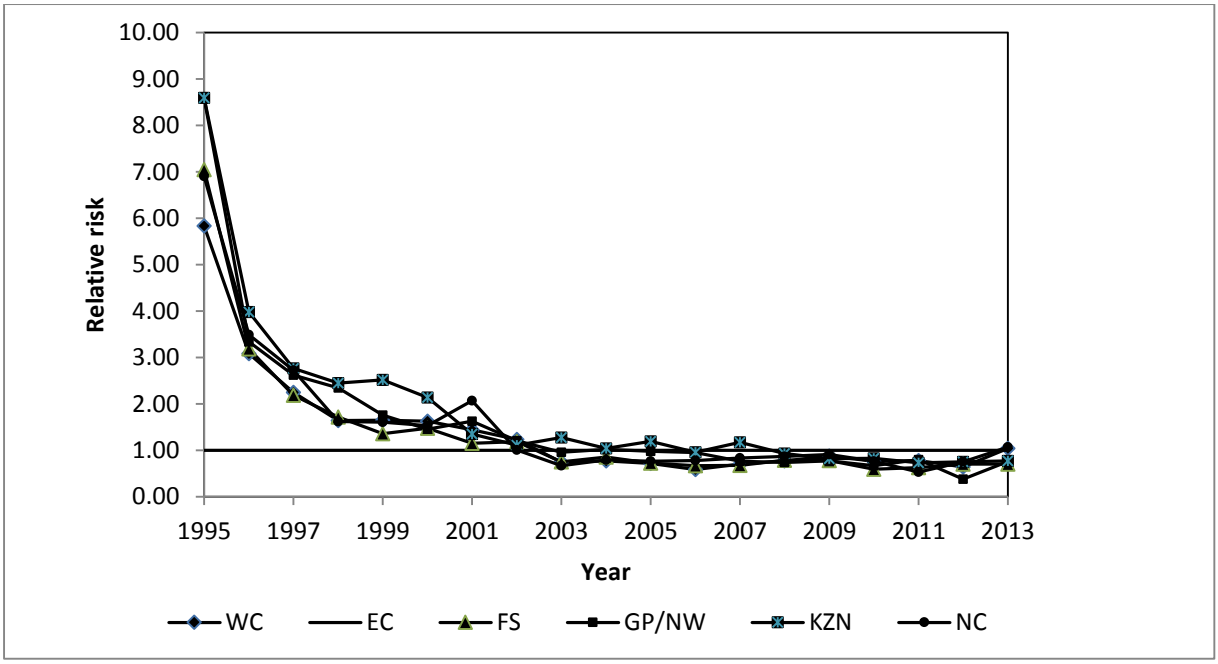

Figure 3.6 Estimated relative risk values for region (WC=Western Cape; EC=Eastern Cape; FS=Free State; GP/NW=combined Gauteng & North Western; KZN=KwaZulu Natal; NC=Northern Cape) by year of calving (1995 – 2013) with the Eastern Cape as reference

Table 3.10 Average length of productive life for cows that calved for the first time in 2000 in the six regions

Region	Record status	Number of records	Mean LPL (days)	Maxinum	Proportion censored (%)
Eastern Cape	Censored	639	689	2561	42.04
	Uncensored	881	709	2562	
Free State	Censored	495	854	2702	27.83
	Uncensored	1248	796	2623	
Gauteng/N. West	Censored	731	883	2695	28.56
	Uncensored	1829	778	3776	
Kwa Zulu Natal	Censored	535	913	2738	36.60
	Uncensored	928	964	2833	
Northern Cape	Censored	565	933	2766	41.36
	Uncensored	801	930	2681	
Western Cape	Censored	1438	958	2748	44.30
	Uncensored	1808	803	2543	

3.4.4.3 Within-herd milk yield class x number of lactations

The risk of culling for older cows, with two or more lactations, was evaluated together with that of younger cows that only had a single lactation. Figure 3.7 shows the estimated relative risk values for cows for within-herd milk production class x number of lactations. Older cows had a relatively higher risk of being culled than the younger cows for all classes of milk production class. This was not as unexpected as it reflected the overall culling policy among dairy farmers to retain younger cows than the older cows. This is despite the fact that younger cows are still growing and need a lot of costly high value feeds for growth and production. The assumption is that the rearing costs associated with younger cows could be offset by the high income from the mature cow in the long term. The relative risk of culling of older cows with multiple lactations averaged 1.1703 times that of younger cows with a single lactation.

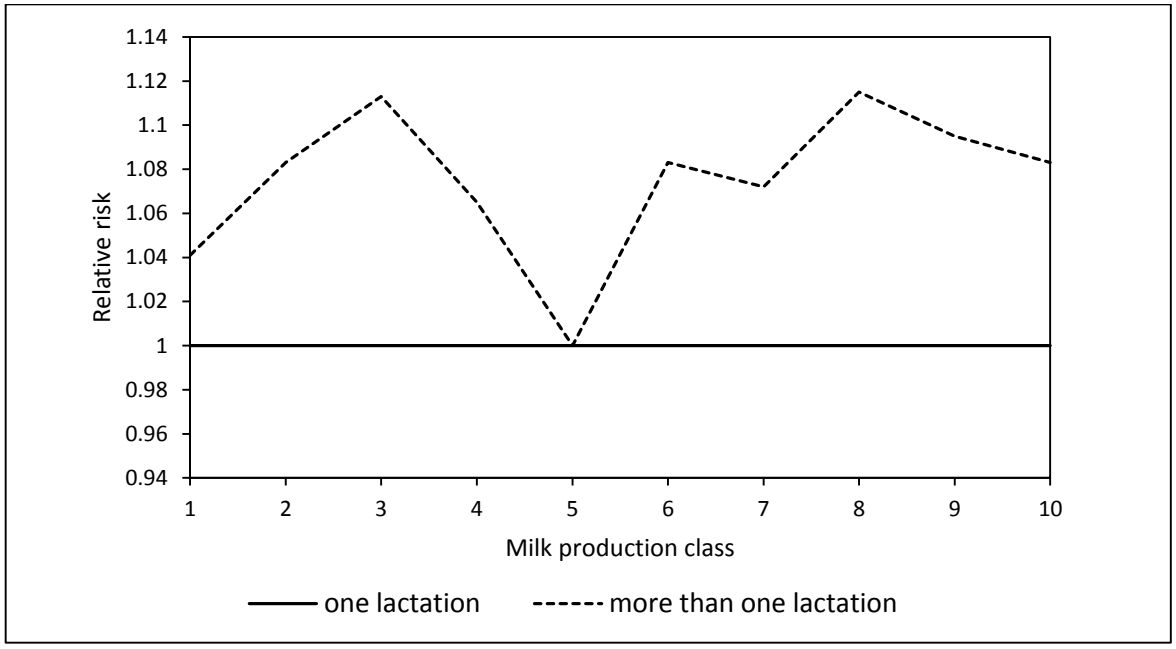

Figure 3.7 Effect of number of lactations on relative risk of culling of older cows and younger cows set to 1.

3.4.4.4 Within-herd milk production class x year-season

Within-herd milk production class had the largest contribution to the risk of culling in herds. Milk yield has constantly been the major culling reason among dairy farmers as indicated by the near constant relative risk (approximate line of best fit) through the years. Figure 3.8 shows the estimated relative risk ratios for two best classes (classes 9 & 10) and worst classes (classes 1 & 2) of milk yield within year-season. Cows with production in class 1 (worst cows) were consistently at relatively very high risk of being culled throughout the year-seasons than those in other classes. Dips in culling risk for especially class one coincided with summer season (season 1) until up to 2011. Cows in classes 9 and 10 (best producers) had a relatively

low risk of being culled (consistently below the reference class). Higher yielding cows tended to stay longer in herds than their low producing counterparts.

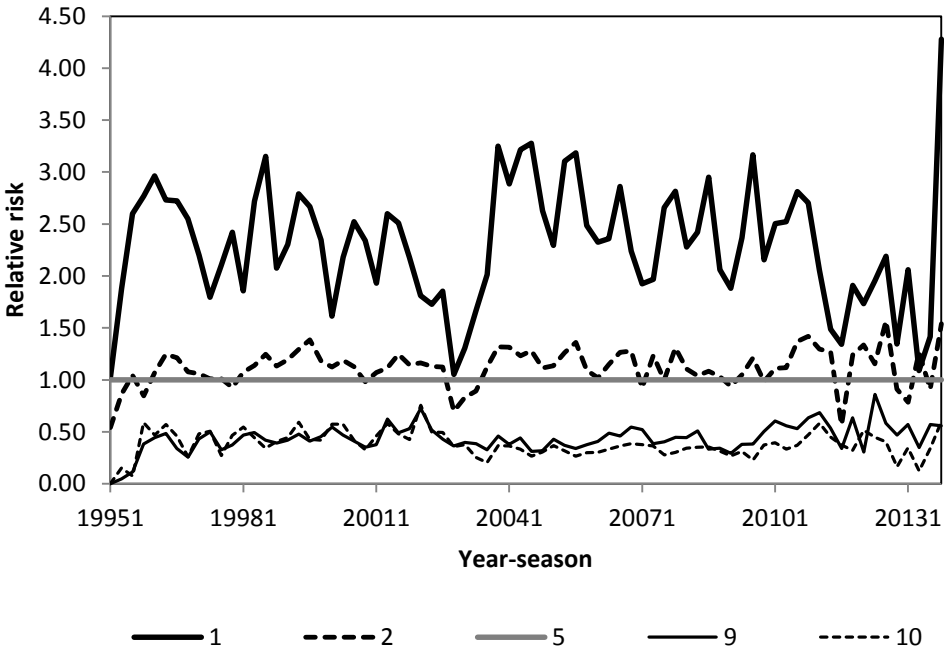

Figure 3.8 Estimate of the relative risk of culling for the worst two (classes 1 & 2) and the best two classes (classes 9 & 10) of milk production class by year-season (reference class 5)

3.4.4.5 Year of calving x within-herd butterfat and protein percent production class

Within-herd protein and fat production percent class were the respective third and fifth most important covariates influencing the probability of an animal being culled from herds. Both good and poor producing cows were at higher risk of being culled for fat and protein percent post-1997 than they were before this period as indicated by an increase in relative risk over the years. Figures 3.9 and 3.10 show the trend in culling risk for protein and butterfat over the years.

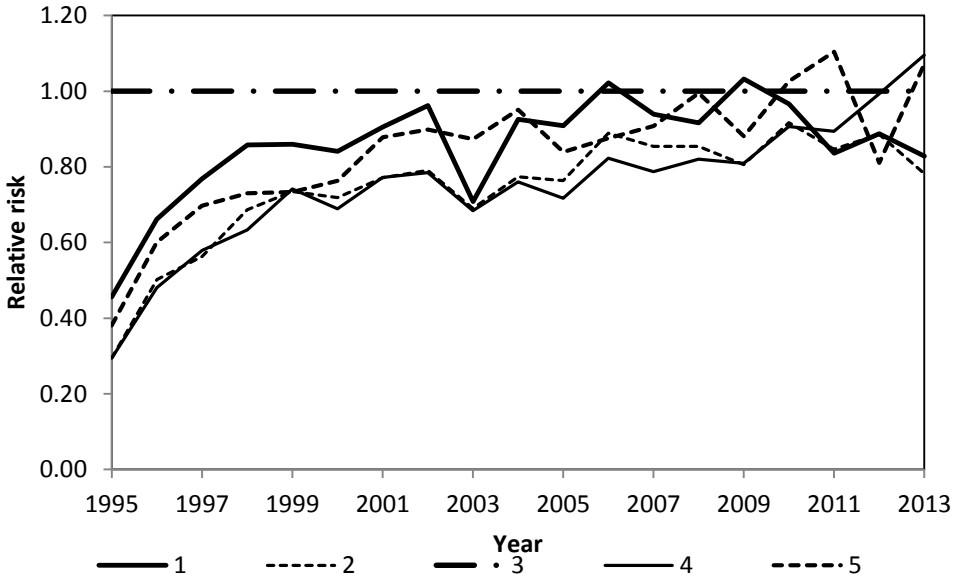

Figure 3.9 Change in relative risk of culling of cows for within-herd fat production percent class (1=bottom 20% production level & 5=top 20% production level) from 1995 to 2013

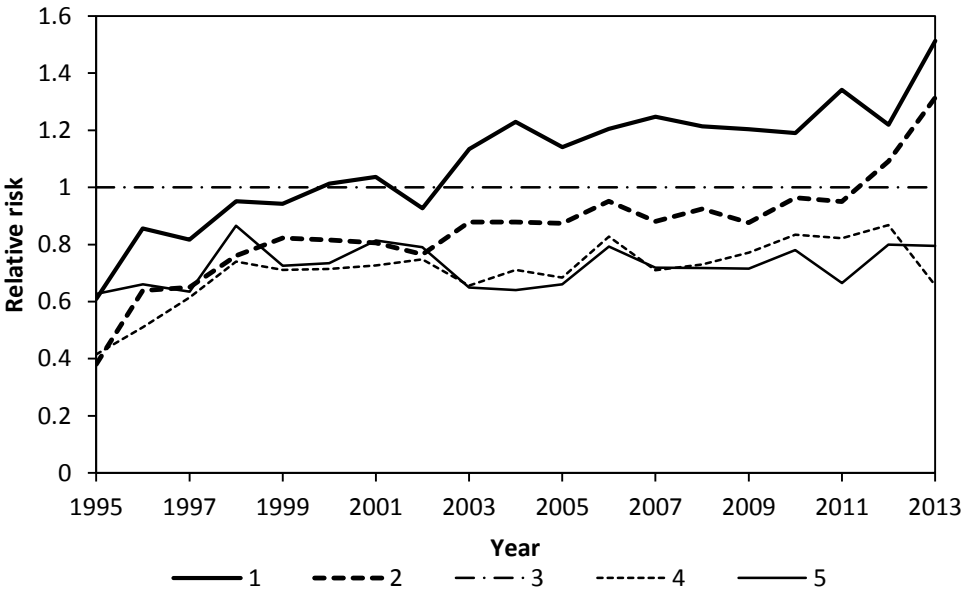

Figure 3.10 Change in relative risk of culling of cows for within-herd protein production percent class from 1995 to 2013 (1=bottom 20% production level & 5=top 20% production level)

Figure 3.11 shows the change in relative risk values obtained by subtracting the relative risk of cow culling in 1995 from that of 2013 to determine the biggest change in the probability of culling on the basis of both butterfat and protein. There was a marked increase in the risk of culling of cows on the basis of low protein percent content among the lower producing classes

(classes 1 and 2). Similarly, high protein and fat percent producing animals (classes 4 and 5) were increasingly being culled for butterfat percent than they were in 1995. Fat percent has been an important culling criterion from 1995 though.

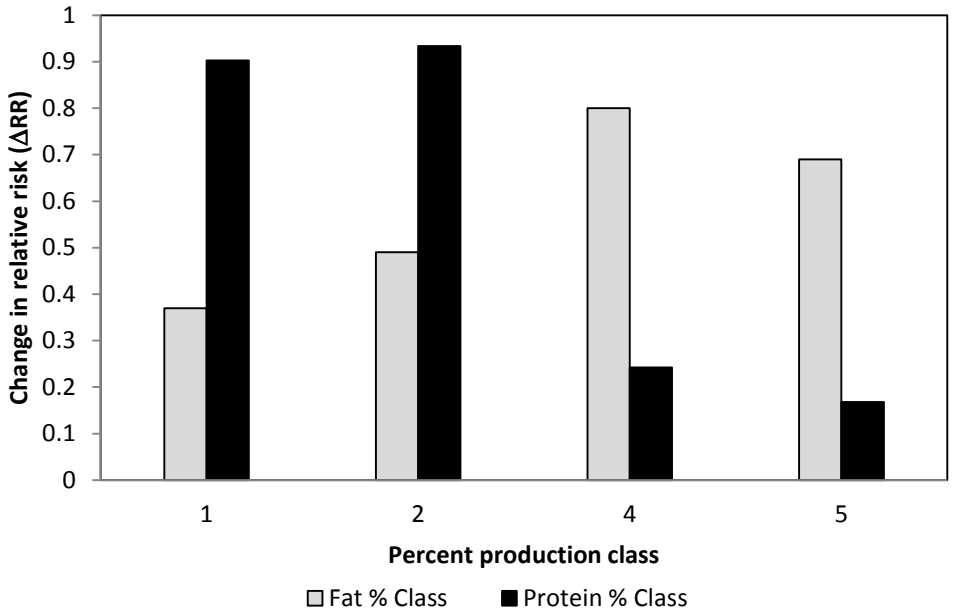

Figure 3.11 The change in relative risk for cows for the period 1995 to 2013 for protein and butterfat percent class.

3.4.4.6 Annual herd size change x herd size

Herd size changes were estimated in small herds (less than 5 cows and 5 – 20 cows), medium sized herds (20 – 49 cows) and large herds (> 50 cows). The risk of culling was low for small herds and was highest in shrinking large herds. Table 3.11 shows the relative risk ratios for small herds and Figure 3.12 shows variations in relative risk ratios with class of herd size change for the larger herds (> 50 cows). Cows in commercial herds had a lower relative risk (RR=0.794) of being culled than those in registered herds (reference class) probably due to intense selection usually associated with the latter as they were breeding herds.

Table 3.11 Estimated relative risk ratios for annual herd size change in small herds

Herd size (cows)	Class	Range of change (%)	Relative risk
Less than 5	1	-	0.748
5 to 19 cows	2	< - 10.	0.616
	3	-10 to 10	1.318
	4	>10	1.311

Cows in stable small herds ranging in size from 5 and 19 were marginally most likely to be culled whilst those in shrinking small herds were at the lowest risk of culling than all animal in the population. In the larger herds, cows were most likely to be culled in shrinking herds than in expanding herds. The latter herds actually expand because cows stay in production in these herds for a longer period than in the former in which probably they are culled as they dry off.

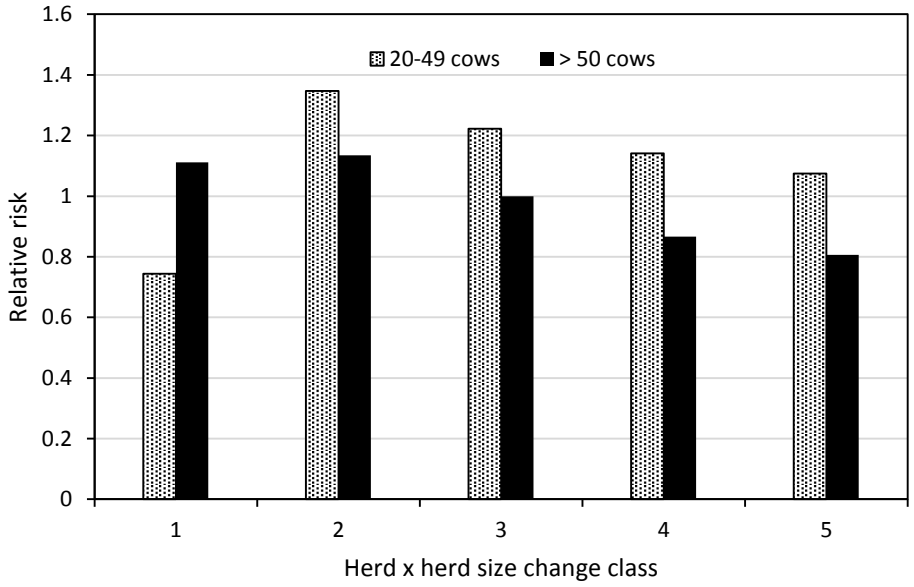

Figure 3.12 Estimated risk ratios for herd size change (%) by herd size variation

3.5 Discussion

3.5.1 Age at first calving

A negative relationship was observed between age at first calving and functional longevity. The biggest jump in culling risk was observed among older heifers. Heifers that calved at 42 months of age were 1.763 times at greater risk than those calving at 24 month of age implying that older heifers were more predisposed to culling than younger ones. This was consistent with results of studies carried out elsewhere (Strandberg and Roxstrom, 2000; Ducrocq, 2005; Sewalem *et al*., 2005; Terawaki and Ducrocq, 2009; Raguz *et al*., 2011). Delayed onset of reproduction and the subsequent late calving among heifers is usually a consequence of

suboptimal management of the dairy animal particularly feeding and reproduction, as well as unexpected events such as abortions (Durr *et al*., 1999). This implies increased rearing costs which may not be recoverable even if the animal were to have a very good first lactation milk yield. When a cow commences reproduction late in life, its lifetime production performance may not be realised since it will be limited in terms of maximum number of lactations it can have as well as the average lactation length (Sasaki, 2013). In this study, heifers calving early at 20 months of age were marginally at a higher risk (relative risk=1.015) of being culled than heifers calving at 22 (relative risk=0.962) and 23 months of age (relative risk=0.990). Other studies reported similar trends in Canadian dairy cattle (Sewalem *et al*., 2005) and Japanese Holsteins (Sasaki, 2013). This was attributed to problems relating to difficulty in calving in younger heifers, low milk production and general poor body condition all of which are consequences of poor feeding and reproduction management. The results from this study contradicted those by Ducrocq (1994), Ojango *et al*. (2005) and Jenko *et al*. (2013) who reported non-significant effect of age at first calving on functional longevity. This was probably due to differences in target age at first calving between different herd management systems (Bielfeldt *et al*., 2006). Moreover, the main determinant of age at first calving is the pre-pubertal growth rate which depends on both the environment and the genotype of the animals (Wathes *et al*., 2008).

3.5.2 Region x year of calving

Relative risk of culling showed a gradual decrease over the years across all the regions. Broadly, there were systematic differences between regions observed outside the Eastern Cape in which animals were consistently at higher risk of being culled over the years. Against expectations, risk was lowest among cows in the Northern Cape and Western Cape Provinces. This was probably because of differences in systems of production. A significant number of farmers in the Western Cape and Northern Cape Provinces are rearing cows on total mixed rations with minimal or no pasture grazing. The cows are provided with all year intensive housing system. This is mainly to protect them from seasonal variations in weather elements that interfer with sustainable dairying. Areas further to the north of South Africa, Kwa Zulu Natal, Gauteng and North Western provinces are drier and cows are reared predominantly on pasture with supplementation. This obviously influences longevity. Ducrocq (2005) noted clear differences between the Western and Southern regions of France. The magnitude of the difference was small (0.65 – 1.13) as was observed in the magnitude in the current study. Jenko *et al* (2013) also reported significant influence of region on longevity of Slovenian cattle as did Raguz *et al*. (2011) in Croatian dairy, Chirinos *et al*. (2007) in Spanish Holstein-Friesian cattle and Smith *et al*. (2000). This was attributed to differences in level of intensification of dairying (Raguz *et al*., 2011) with cows in regions with low intensification of dairying being at

the lowest risk of being culled just as those in regions with predominantly small herds (Jenko *et al*., 2013). In Slovenia, the risk of culling was reported low in regions with conditions that did not favour cattle breeding (Jenko *et al*., 2013). This was probably because the farmers restricted culling to increase the milk quota for optimisation of returns.

3.5.3 Production x year of calving

The probability of cows being culled, in the current study, was observed to be higher among low yielding cows than the average cows. For the low yielding cows, a decrease in culling risk was noted to coincide with season 1, the wet, summer period. Pasture will be generally in good condition during this period and as such, most animals tend to perform relatively well with the probability of low yielding cows also increasing production. It reduces their predisposition to culling, albeit for the noted seasons only. Generally, high yielding cows tend to stay longer in herds than low yielding cows. Studies with Japanese Holstein (Terawaki and Ducrocq, 2009), Kenyan Holstein (Ojango *et al*., 2005), Croatian Holstein and Simmental cattle (Raguz *et al*., 2011) and New Zealand dairy cattle (Berry *et al*., 2005) reported similar trends. This can be attributed to the milk payment system that is primarily based on milk quantities supplied to the processors. To the contrary, later study with Japanese Holsteins reported high relative risk of culling in the high yielding cows than the low producers (Sasaki, 2013). This was probably due to differences in statistical models since the latter fitted stage of lactation within milk yield class as well as the differences in herd management.

The estimated relative culling risk associated with butterfat and protein percent production has increased with time through the years as farmers emphasized more on selection based on these two traits. The shift towards fat and protein percent production and the gradual increase in relative risk of culling associated with these two traits from mid-1990s coincided with the adoption of the Holstein Breeding Value Index (BVI) by the South African Holstein Society in 1995 (Taurus Holstein, 2002). This index was biased towards the high protein and butterfat producing cows with large framed and extremely angular bodied cows with tightly attached udders (Banga, 2009). Further revision of the BVI significantly reduced emphasis on protein relative to fat. However, the two traits remained part of the Holstein selection index though (Taurus Holstein, 2007). Despite increased emphasis on fat and protein content, milk yield remains the most important criterion for culling cows in dairy herds.

The change in -2 log likelihood indicated that protein percent production contributed more to culling decisions than fat percent production. This was as expected because in South Africa, farmers are paid more on protein content than on fat content for some payment schemes. The culling policy of most dairy herds is primarily influenced by the milk producer prices. The

pricing system in South Africa has been liberalised and processors can get into desirable contracts with producers. As such, producers will put emphasis on those parameters that bring them more income from milk sales. The difference in relative ratios between the different milk classes (0.263 to 2.8) were much higher than differences between estimates of risk for protein (-0.089 to 0.492) and butterfat percent (0.07 – 0.393) implying that farmers tend to cull cows more on total production than protein and butterfat (Chirinos *et al*., 2007). This makes milk yield the most important criterion for culling among South African Holstein herds as reported elsewhere (Smith *et al*., 2000; Sewalem *et al*., 2005; Mészáros *et al*., 2008; Raguz *et al*., 2011).

3.5.4 Stage of lactation and number of lactations

Estimates of the Weibull shape parameter for within-parity stage of lactation indicated a low relative risk of culling for cows in the early to mid-lactation (DIM=0 to 270 days) and elevated risk for the later stage of lactation (DIM=271 to 380 & DIM>380 days) for all lactations. The risk of culling was highest during the period 271 to 380 days after calving. This was broadly consistent with findings by Terawaki and Ducrocq (2009) albeit with different definition of the stages of lactation. In the current study, the risk of culling was highest during 271 to 380 days after calving whilst Terawaki and Ducrocq (2009) observed highest risk within an almost corresponding period of 250 to 350 days after calving. Most farmers cull poor performers at the end of the lactation which on average is at the end of 305 days of lactation. This falls within the period 271 to 380 and as such risk of culling was highest during this period. Beyond 305 days of lactation, most animals still in production will be those that may have failed to conceive after the last calving but still maintaining high levels of production. Farmers will most likely extend the lactation period of these animals before they are eventually culled for fertility reasons. The fact that risk was low during the fourth stage of lactation (dry period) could be due to the farmers' culling policy which is based mainly on yield. During the fourth stage of lactation, animals will be dry thereby providing little basis for culling unless they have other health related issues such as injuries, abortions or chronic mastitis which would influence the next lactation.

The probability of being culled was consistently higher for cows with multiple lactations than those with a single lactation. This could be due to the overall culling policy among South African Holstein dairy farmers which favours younger cows to older cows. Farmers would rather retain a young cow with superior genetic merit for production than an older cow with lower genetic merit and declining production. This is despite the high costs of rearing young cows in terms of supply of a costly high plane of nutrition and general management requirements.

3.5.5 Herd size x annual herd size change

Annual herd size changes found in this study were realtively high. A considerable number of herds experienced annual herd size changes of up to 50% implying huge variation in the number of milking cows within the herds with time. This could have been caused by either errors of recording of extreme herd downsizing both of which would need to be verified. The trend of annual herd changes were similar for medium sized herds (21 to 50 cows) and large herds (more than 50 cows). In these herds, risk of culling was highest in shrinking herds (RR= 1.2) compared to expanding herds (RR=0.8). Cows in larger herds were more predisposed to culling than those in smaller herds (Smith *et al*., 2000) and this would explain the low culling risk for cows in small herds. High relative risk ratios for shrinking herd were also observed in Japanese Holsteins (Terawaki and Ducrocq, 2009), Spanish Holstein Friesians (Chirinos *et al*., 2007) and Slovenian Brown cattle (Jenko *et al*., 2013). Farmers with small herds are not very much inclined to cull cows even for low production in view of the implications it would have on their income base. As such, animals in such herds will have a low probability of being culled as was observed in the current study study.

The herd size variation in South African Holstein herds was very high. This could be difficult to account for in analyses. Some proportional hazards models account for this huge variation through incorporation of herd-year-season as a fixed effect in the model since it has been reported to account for changes in annual herd sizes (Chirinos *et al*., 2007). The current study evaluated the combined effect of herd size and annual herd size in the model. This was because the effect of herd size as a stand-alone effect influences functional longevity differently in small and large herds. Raguz *et al*. (2011) included the effects of herd instead of herd size variation with time in their model to solve this problem. However, Ducrocq (2005) proposed a way of appropriately handling this phenomenon and it is currently being implemented in the evaluation of French dairy cattle for longevity. Annual herd size changes were classified according to herd size and comparisons made within-herd size class. Small herds were regarded as stand-alone classes regardless of whether their size was increasing or decreasing. This was the approach adopted in the current study.

3.6 Conclusion

A proportional hazards model used in the current study evaluated the combined effects of stage of lactation within parity for parity one and combined parities beyond one, year within region, milk production class within year-season, within-herd fat and protein percent production per year, annual herd size change by herd size, herd status as well as age at first calving. Herd effects were accounted for in the annual herd-size change x herd size variable

just as year effects were incorporated in year-season. Milk production, fat and protein percent had the greatest impact on functional longevity. Low producers in terms of milk yield, protein and fat percent had the greatest risk of being culled from herds. Other covariates, though important, did not have a large effect on culling risk as indicated by the small variation from the average cows. Region had the least impact on culling risk indicating no particular culling trends across regions. Age at first calving only became important at older ages as a determinant of culling risk and had therefore low impact. Cows in registered herds were more likely to be culled than those in commercial herds just as cows from larger herds were at higher relative risk of being culled than animals from small herds. In large herds, relative risk was high in shrinking herds. Having identified these fixed effects influencing longevity in South African Holsteins, there is scope for adjusting for these in genetic evaluation of the trait in Holsteins.

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CHAPTER 4

Genetic parameters for longevity in the South African Holstein cattle from proportional hazards models

4.1 Abstract

A piecewise Weibull proportional hazards sire-maternal-grandsire model was used to estimate genetic parameters and sire breeding values for functional longevity in South African Holstein cattle. Data consisted of records of 161 222 of daughters of 2051 sires calving between 1995 and 2013. Analysis was done with the Survival Kit v6. Functional longevity was defined as the number of days from first calving to culling or censoring. The model had random herd-year, sire and maternal grand sire effects, fixed time-independent effects of age at first calving, fixed time-dependent effects of region by year, number of lactations by within-herd class of milk production, year by season by within-herd milk production class, within-herd protein and fat percent classes by year and herd size by annual variation herd size class. Different Weibull baseline hazard functions over four periods and five lactations: 0 to 270 days, 271 to 380 days, 381 to drying date and dry period until next calving were estimated. The effective heritability estimate was 0.108. Individual sire breeding values ranged from -4.80 to 2.12 for worst and best sire respectively. Average sire breeding values showed an overall decrease of 1.35 standard deviation from 1981 to 2007. Equivalent heritability estimates were lower than effective heritability but increased with the number of uncensored daughters per sire. Genetic parameters obtained in this study were higher than previous estimates obtained for the South African dairy cattle with linear models. There are opportunities for including the trait in the Holstein Profit Ranking Index currently being used to rank and select South African Holstein cattle.

Keywords: survival analysis, piecewise Weibull model, hazard rate, effective heritability

4.2 Introduction

South African Holstein cattle are currently selected on the basis of the Holstein Profit Ranking (HPR) index that includes breeding values and economic values for production traits, calving interval and somatic cell count. More functional and fitness traits have been identified for inclusion in this HPR index to improve the accuracy of estimation of the net genetic merit of the animals. The immediate candidate trait for inclusion, in view of its economic importance, is functional longevity, also called the length of productive life (LPL). Estimates of its economic values in both concentrate and pasture based Holstein dairy systems in South Africa have

indicated favourable economic values for longevity (Banga, 2009). The estimates were comparable to those for milk yield and butterfat and higher than those for somatic cell count and calving interval when standardised to protein. A framework for routine estimation of these economic values for longevity is already in place. However, objectively determined breeding values still need to be estimated for this trait in Holsteins.

South African dairy cattle breeds have been genetically evaluated for longevity with linear animal and sire multivariate models in Jersey cattle (du Toit, 2011), bivariate animal model in Holsteins (Setati *et al*., 2004), threshold linear models Angus cattle (Maiwashe *et al*., 2009) and random regression models in beef cattle (van der Westhuizen *et al*., 2001). These methods have and are currently being used elsewhere. Random regression models have been used in evaluation of Canadian Simmental (Jamrozik *et al*., 2001), British Holsteins (Veerkamp *et al*., 2001) and Dutch dairy cattle (van Pelt & Veerkamp, 2014). Boettcher *et al*. (1999) and Kern *et al*. (2014) used threshold models for Canadian and Brazilian Holsteins respectively, whilst numerous other studies have used linear models (e.g. Zavadilová *et al*., 2009; Zavadilová & Stipkova, 2012; Wielbelitz *et al*., 2014). Estimates of heritability obtained with random regression models were low and ranged between 0.002 to 0.36 (Jamrozik *et al*., 2001; Veerkamp *et al*., 2001; van Pelt & Veerkamp, 2014) whilst heritability estimates from linear models ranged from 0.001 to 0.06 (Setati *et al*., 2004; Holtsmark *et al*., 2009; Zavadilová *et al*., 2009; du Toit, 2011; Zavadilová & Stipkova, 2012; Wielbelitz *et al*., 2014). Heritability estimates from threshold models were slightly higher than estimats from random regression and linear models. They ranged from 0.04 to 0.15 (van der Westhuizen *et al*., 2001; Gonzalez-Recio & Alenda, 2007; Holtsmark *et al*., 2009; Kern *et al*., 2014). Even were the estimates were relatively high, the methods used to derive may not have been able to appropriately handle survival data by virtue of its nature.

Proportional hazards models have increasingly been adopted for the evaluation of functional longevity in dairy cattle (e.g. Caraviello *et al*., 2004a & 2004b; Terawaki *et al*, 2006; Mészáros *et al*., 2008; Terawaki & Ducrocq, 2009; M'hamdi *et al*., 2010; Jovanovic & Raguz, 2011; Jenko *et al*., 2013). These models are based on the hazard rate concept which represents the instantaneous risk of a cow being culled at time ***t*** (days) after calving or the probability of being culled or dying at time t given that the cow was still alive just before culling or death (i.e. at time ***t-1***). The hazard rate is the product of the baseline hazard rate and the exponential function of a number of fixed and random effects, referred to as covariates (Bünger & Swalve, 1999). More than 50% of the 20 countries on Interbull that were carrying out national evaluation of sires for functional longevity as of 2014, were using the proportional hazards sire or sire-maternal-grandsire models. Previous critiscism of proportional hazards models were

that they could not account for non-random mating among animals (Jairath & Dekkers, 1994; Boettcher *et al*., 1999). Besides, the commonly used software for survival analysis with PH models currently only use univariate analyses (Veerkamp *et al*., 2001; Holtsmark *et al*., 2009) and therefore unable to adjust for correlations between traits. Use of the sire-maternal-grand-sire models in Survival Kit has been criticised for ignoring the contribution of the cows mated to these sires to the performance of the daughters especially when there is assortative or disassortative mating. Because of this, proportional hazards models maybe considered optimal in a statistical sense but they, in fact, may not be economically optimal (VanRaden *et al*., 2006). Despite these limitations, proportional hazards models have become the method of choice for analysing survival data. The benefits of proportional hazards models over the classical linear models include their ability to use specialised distributions such as the Weibull and exponential which are more relevant to failure time data whilst at the same time making appropriate adjustments for time-dependence of some variables (Caraviello *et al*., 2004b; Ducrocq, 2005). They are also able to handle both complete and incomplete records in an appropriate way. Just like the mixed linear models, PH models can also be extended to include random genetic effects (Ducrocq, 1997).

Estimates of heritability for functional longevity can be estimated either on a logarithmic or original scale. The former is useful in situations where data is transformed on a linear scale and assuming normality of the random variable (Yazdi et al., 2002). Unfortunately, this may not be a very efficient method of using the data to estimate the parameters. Heritability estimates on the original scale, herein called the effective heritability, are therefore more preferable. Estimates of effective heritability have been reported to average between 0.09 to 0.22 (Ducrocq, 1997; Bünger & Swalve, 1999; Egger-Danner *et al*., 2005; Caraviello *et al*., 2004a). The wide variation in heritability estimates for animals in different regions and countries can be attributed to reasons including differences in the accuracy of sire identification, record keeping (Caraviello *et al*., 2004b) and the precision of data analyses. This study was carried out to determine the heritability estimates for functional longevity and predicted breeding values for sires in South African Holstein cattle.

4.3 Materials and methods

4.3.1 Data

Holstein data comprising of production, pedigree, dates of birth and calving, herd status, region and herd code were obtained from the INTERGIS of the National Milk Recording and Improvement Scheme. The data were subjected to edits and preparation using SAS Version 9.3 (SAS, 2002 – 2010) and FORTRAN 90. Details of edits and preparation are as presented in Chapter 3 (Section 3.2.1). The records were from cows that were progeny of sires with

daughters in herds with at least five animals. Only records for cows calving for the first time between 1 January 1988 and April 2013 were included in the analysis. Data consisted of complete and incomplete records. Complete records had an exit code and incomplete records were for cows that were still in production and did not have exit codes. Cows calving for the first time before 1 January 1988 were excluded from the analysis and cows with lactation observations after April 2013 but with less than six calvings were considered as censored.

All cows still alive at the end of the fifth lactation were censored at end of the fifth lactation. This was to allow analysis to focus on culling events occurring in early life of the animals since these have a direct bearing on profitability of dairy farming. Cows with unknown exit codes were considered censored at the end of the last known lactation and those with missing exit codes were considered culled at the last known date of their last lactation. There were no records of animals that changed herds during their lifetime. Heifers younger than 20 months and older than 42 months at calving were excluded from the analysis. The final data set used in the analysis consisted of 161 222 records of daughters of 2051 sires without any truncated records. The latter implied that only records of cows that calved for the first time after 1 January 1988 were included in the analysis. A total of 65 227 (40.46%) records were censored. The average within-lactation censoring and failure times for censored and uncensored records were 258 and 261 days respectively. Productive life was defined as the number of days between first calving and the last known lactation end date.

4.3.2 Estimation of the survival and hazard function

The Kaplan-Meir estimates were determined with the non-parametric Cox proportional hazards model stratified by either herd status or region. Estimates obtained were used to plot the survivor and hazard functions.

4.3.3 Estimation of variance components

Variance components, Weibull shape parameter (ρ) and the parameter of the log-gamma distribution of random effects (γ) were estimated with the Survival Kit v6 program (Ducrocq *et al*., 2010). Empirical within-lactation estimate of the overall hazard function derived from the Kaplan-Meir estimate of the survivor curve (Kaplan & Meir, 1958; Kalbfleisch & Prentice, 1980) has shown different slopes for lactations longer than 380 days (Figure 3.1). The model used in the analysis was as explained in section 3.2.4 and Table 3.6. This can be generalized as: -

$$\lambda(t)=\lambda_{0,ls}(t)\exp\{hy_k(t) + \Sigma_m f_m(t) + s_i + 0.5\ mgs_j\}$$

In the model, t was the time from first calving to culling or censoring. $\lambda(t)$ was the hazard function of daughter ***k*** of sire ***s*** with recorded herd life of ***t*** days and hy_k was the random herd-year effect which was assumed to be independently distributed following a log-gamma distribution with both the shape and scale parameters equated to γ so as to force the mean to be 1. $\boldsymbol{\lambda_{0,ls}(t)}$ is the piecewise Weibull baseline hazard function for the nth stage of lactation (n=1, 2, 3, 4) of the rth lactation (r=1, 2, 3, 4, 5) started in 1988 to 2012 with scale parameter τ and shape parameter ρ and ***T*** is the time (in days) between the most recent calving and current time and $\Sigma_m f_m(t)$ is the sum of all fixed effects as described previously in Table 3.6.

The gamma parameter of the combined effect of herd-year was jointly estimated with other fixed and random effects after the algebraic integration of the log-gamma herd-year random effect. The sire variance was estimated as the mode of its posterior density (probability distribution) as approximated by the Laplacian integration (Ducrocq & Casella, 1996, Ducrocq *et al*., 2010). The mean, its standard deviation and skewness of the posterior density were obtained from survival kit and were subsequently used to plot the posterior density of the variance component using a Gram-Charlier approximation. The obtained standard deviation of the posterior probability distribution from Survival it can appropriately be considered as a conservative estimate of the standard error.

4.3.4 Genetic parameters for longevity

4.2.4.1 Heritability estimates

Effective and equivalent heritability were both estimated in the current study. The former represents heritability in the absence of censoring and therefore does not depend on Weibull parameters (Yazdi *et al*., 2002) and is usually higher than the latter. The heritability values were estimated from the obtained variance components for the random herd-year and sire effects. The sire-maternal grandsire effect was considered random and assumed to account for all the genetic variance including those emanating from the ancestors. Effective heritability estimates were computed using the following method adapted from Jenko *et al*. (2013): -

$$h^2 = \frac{4\sigma_S^2}{\frac{5}{4}\sigma_s^2 + \Psi^{(1)}(\gamma)+1} \quad \textbf{(4)}$$

where: h^2 is the effective heritability estimate;

σ_S^2 is the additive genetic variance;

$\Psi^{(1)}(\gamma)$ is the variance of the log-gamma herd-year effect;

Equivalent heritability was estimated according to Yazdi *et al*. (2002) as modified by Jenko *et al*. (2013). This takes into consideration the influence of the proportion of censored observations at a specified time and is therefore more realistic. Equivalent heritability was estimated using the Kaplan-Meir estimate of p(t) for the first five lactations of the productive life of the cows using the following formula: -

$$h_e^2 = \frac{\sigma_S^2}{\frac{5}{4}\sigma_S^2 + \Psi^{(1)}(\gamma) + \frac{1}{p(t)}} \quad \textbf{(5)}$$

where: h_e^2 is the equivalent heritability estimate;

σ_S^2 is the additive genetic variance;

$\Psi^{(1)}(\gamma)$ is the variance of the log-gamma herd-year effect;

p(t) is the proportion of uncensored records;

4.3.4.2 Breeding values

Solutions for sire effects from the Weibull frailty model were used to estimate and standardise the breeding values of the sires as follows: -

$$EBV_{sire} = -\left(\frac{s - \bar{s}}{\sqrt{\sigma_S^2}}\right) \quad \textbf{(7)}$$

where: **s** is the estimate of sire effects;

$\bar{s}$ is sire effects of a group of base sires (reference sires);

σ_S^2 is sire variance.

4.3.4.3 Reliability

The effective heritability estimates from the survival analysis were used to determine the estimated reliability (R) of the sires proofs based on the number of their uncensored daughters using the following formula (Ducrocq, 1999; Yazdi *et al*., 2002; Mészáros *et al*., 2008; Jenko *et al*., 2013):

$$R = \frac{n_u}{n_u + \left[\frac{4 - h^2}{h^2}\right]} \quad \textbf{(6)}$$

where: R is reliability (accuracy of estimation) of the sire proofs for functional longevity;

n_u is the number of uncensored daughters of each sire;

h^2 is the effective heritability;

4.4 Results

4.4.1 Descriptive statistics

Table 4.1 shows the overall descriptive statistics for the entire functional life of the cows. The average length of productive life was relatively higher among the censored cows than the uncensored cows. Maximum functional life was however longer for the latter than the former.

Table 4.1 Descriptive statistics for entire productive life of the animals

Description	Censored	Uncensored
Number of record	65 226	95 994
Maximum length of productive life (days)	2 984	3 068
Average length of productive life (days)	850	771
Minimum censoring/failure time (days)	1	1

4.4.2 Survivor functions

4.4.2.1 Survivor functions by region and herd status

The survivor curves for cows in registered and commercial herds are shown in Figure 4.1. Survival was higher in commercial herds than in the registered herds. There was relatively intense culling in registered herds. Inversely, animals in commercial herds had relatively lower hazards than those in the registered herds.

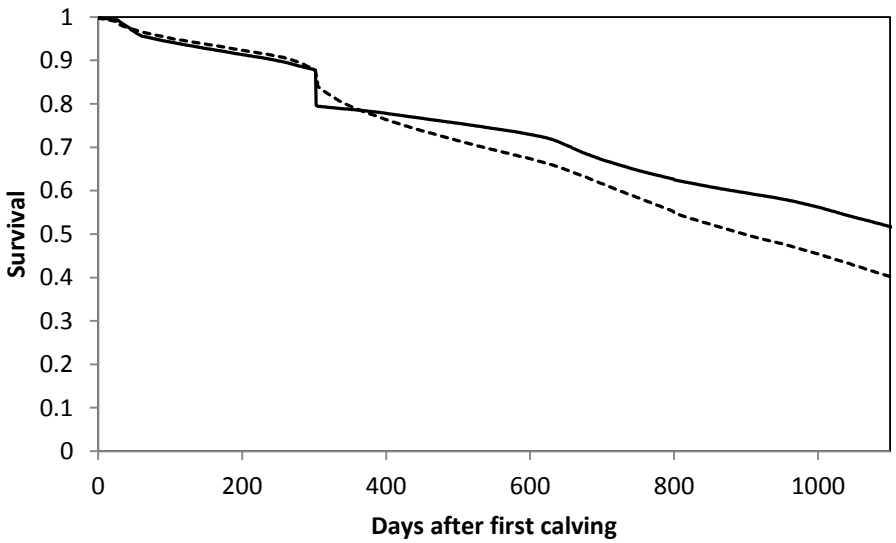

Figure 4.1 Survivor function curves for cows in registered breeding (dotted line) and in commercial Holstein herds (solid line) showing survival by days after first calving for the first three years

4.4.3 Genetic parameters

4.4.3.1 Sire variances and heritability estimates

Effective, equivalent heritability, breeding values and reliability of the estimated breeding values were estimated. The estimates of the gamma parameter, random year and sire variances, variance of the log (gamma) parameter and the effective heritability estimates for functional longevity are in shown in Table 4.2. At 0.109, the effective heritability was relatively low but higher than all estimates previously reported for dairy cattle in South Africa, albeit with different models.

Table 4.2 Parameter estimates for the data

Variable	Value estimate
Gamma parameter	1.94615
Herd-year variance	0.66744
Sire variance	0.04724 ± 0.00171
Effective heritability (σ^2_{eff})	0.109

A plot of Gram-Charlier approximation of the posterior density of the sire genetic variances (Figure 4.2) indicated that sire variance was significantly different from zero with a relatively narrow confidence interval. The trend in equivalent heritability, which is the heritability of the trait taking censoring into consideration, is shown in Figure 4.3. It was initially lower but increased with time after first calving.

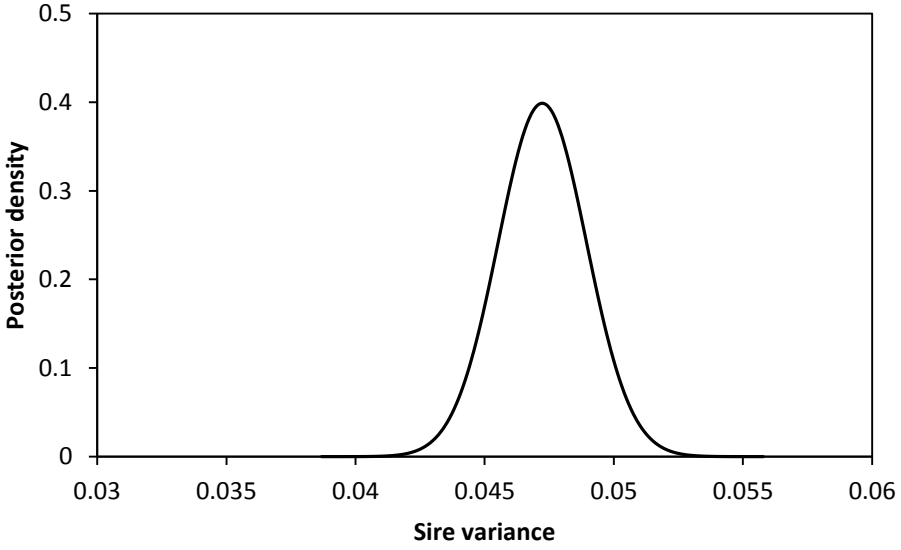

Figure 4.2 Gram-Charlier approximation of the posterior density function for the sire variance

4.4.3.2 Breeding values and reliabilities

The sire proofs ranged from a low of -4.798 (Sire=616 born 1988) to a high of 2.116 (sire=634 born 1987) implying that the daughters of the best sire were more than twice less likely to be culled or die than daughters of the average sire EBV=1.000). Conversely, daughters of the worst sire were 4.798 times more likely to be culled or die than those of the average sire. Reliabilities for the sire-proofs were also plotted as function of the number of uncensored progeny of each sire. Reliability increased with a corresponding increase in the number of uncensored daughters per sire. Figure 4.4 shows the change in reliabilities with number of uncensored daughters per sire.

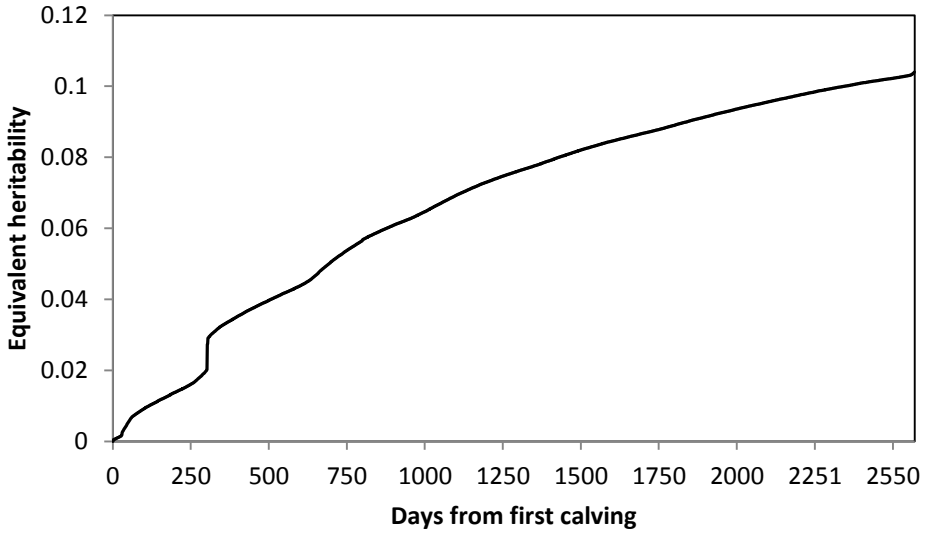

Figure 4.3 Equivalent heritability as function of the days from first calving

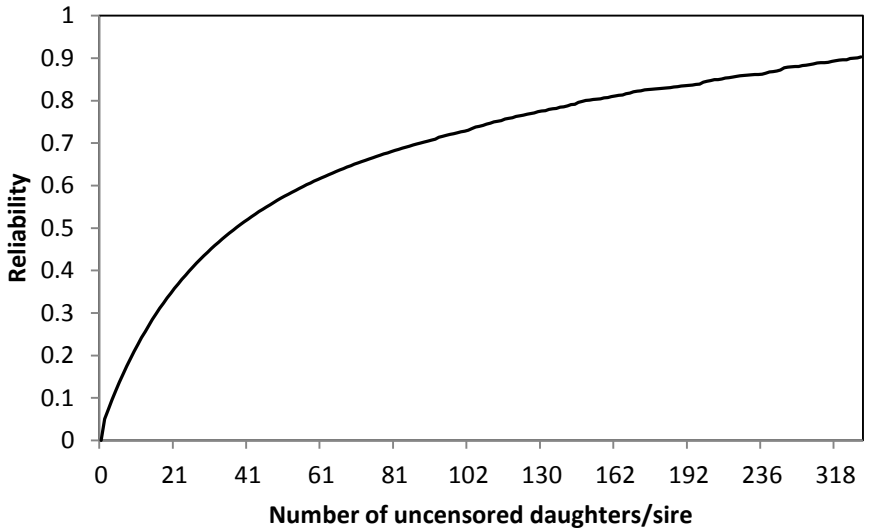

Figure 4.4 Reliabilities for sire proofs as a function of the number of uncensored daughters per sire

Trends in breeding values were obtained by plotting average sire breeding values by year of birth of the sires. Figure 4.5 indicates the trend in average sire breeding values for the period 1981 to 2007 only.

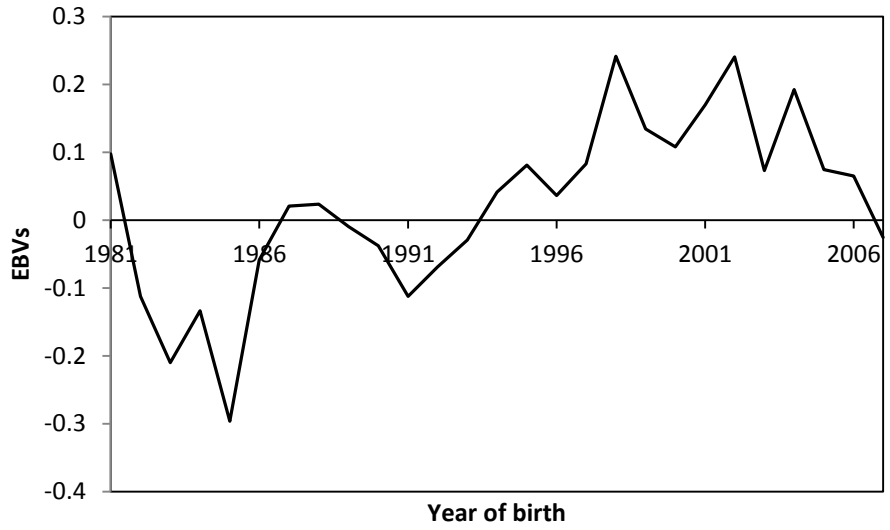

Figure 4.5 Trends in sire breeding values for longevity for the period 1981 to 2007

4.5 Discussion

As was the case with all the other studies using survival models, analysis in the current study was based on the sire-maternal-grand-sire (SMGS) models. The decision to use the SMGS model was mainly because of the amount of time that would be required to run animal models. Survival analysis approximates the posterior density of the sire variances through repeated inversion of the Hessian matrix of the log-posterior density. If animal models are used, this becomes too time-demanding (Mészáros *et al*., 2010). Besides, the Hessian matrix of the log-posterior density is usually sparser than the oft-used mixed model coefficient matrix in linear models due to the presence of time-dependent covariates. This would require elaborate computing resources. With the current increases in computing capacities, animal models can however be aptly applied in survival model analysis.

Previously, proportional hazards models were criticised for assuming that survival, and hence the hazard rate, was the same trait throughout life. This was despite correlation between longevity measures in lactations one to three were reported to be less than one implying the trait was not the same thoroughout life (Holtsmark *et al*., 2009). A piecewise Weibull proportional hazards model was therefore adopted in the current study. This models the hazard rate within lactation on the assumption that the baseline hazard changes at specific times during the lactation of an animal and these hazard rates differ by lactation number.

4.5.1 Genetic parameters

The estimates of heritability obtained in this study were relatively higher (0.109) than previous estimates reported for South African dairy cattle of 0.01 – 0.03 (du Toit, 2011), South African Holsteins of 0.06 (Setati *et al*., 2004) and marginally higher than estimates of 0.08 obtained by van der Westhuizen *et al*. (2001) with South African beef cattle. This was probably because of differences in the models used for analysis. Setati *et al*. (2004) and du Toit (2011) both used linear evaluation of longevity as a non-normal variable analysis. The limitations of these models for longevity analysis have been highlighted elsewhere (Boettcher *et al*., 1999; Roxstrom *et al*., 2003, Sewalem *et al*., 2005; Jamrozik *et al*., 2008). Besides, these previous studies, by adopting the linear models, ignored variation in the culling policy within-herds with time unlike the proportional hazards models that can appropriately handle time-dependence of the variables. The sire variance obtained in this study were withn the range of estimates found among US Holsteins (0.02 – 0.06: Caraviello *et al*., 2004a) but higher than estimates reported for Slovenian Brown cattle (0.028 & 0.031: Jenko *et al*., 2013) and Japanese Holsteins (0.0181 – 0.0441: Terawaki & Ducrocq, 2009). This indicated relatively a lot of variability among the sires for functional longevity in the South African population. It was not unexpected though considering that semen used for artificial insemination among Holstein herds is sourced from more than seven different countries, representing different sire populations. Besides, South African Holstein populations were not directly selecting on functional longevity but rather on production, calving interval and somatic cell count.

The gamma parameter (1.94) from the current study was low and the variance of the herd-year random effect was higher than estimates obtained elsewhere (Terawaki *et al*., 2006). The high variance associated with the herd-year effects in the current study was linked to the high variability among the sires and probably indicated huge variability in within-herd management, and possibly culling, policies among Holstein dairy farmers in South Africa. Despite this high variability in herd-year variance, the estimates of effective heritability from this study were consistent, but on the higher end, with those obtained in French Holsteins (Ducrocq, 2005), Japanese Holstein with inclusion of type scores (Terawaki & Ducrocq, 2009) and Slovenian Brown cattle (Jenko *et al*., 2013). All of which modelled the hazard within lactation unlike previous proportional hazards models (e.g. Ducrocq, 1997) that assumed the hazard for all cows to be constant throughout the entire productive lifetime. By plotting hazard within lactation, this and the other studies (Ducrocq, 2005; Terawaki & Ducrocq, 2009; Jenko *et al*., 2013) demonstrated that hazard varies across lactations and this has to be accounted for during analysis. Using the same principle, Terawaki & Ducrocq (2009) reported higher estimates of effective heritability (0.134) than the ones from the current study mainly because of model and data structure differences. Several earlier studies reported lower estimates of

heritability (Chirinos *et al*., 2007; Mészáros *et al*., 2008; Holtsmark *et al*., 2009) whilst Ducrocq (1997), Sewalem *et al*. (2005), M'hamdi *et al*. (2010) and Sasaki *et al*. (2012) obtained relatively higher estimates than those found in the current study. Most of these differences could be attributable to different types of models and nature of data used in these studies. Some used data from relatively small herds (e.g. Terawaki & Ducrocq, 2009). Individual breeding values for sires for length of productive life ranged from -4.80 to 2.12 for worst and best sire respectively. Positive values indicate superior longevity and negative values poor longevity. Trends showed a decrease in sire breeding values for functional longevity for the period 1981 to 2007. Jenko *et al*. (2013) observed a similar unfavourable trend in Slovenian Brown cattle. This was expected considering that most culling among herds has been on production traits (milk, fat and protein) all of which are known to be negatively correlated to longevity unless the latter is corrected for yield (Jenko *et al*., 2013). Naturally, high yielding cows will be kept in herds for longer than low yielding cows. By implication, selection for high milk yield produces a desirable correlated response in functional longevity.

Estimates of reliability increased with the number of uncensored daughters per sire as was reported elsewhere (Yazdi *et al*., 2002). Such an increase in reliability indicates an increase in the correlation between true and estimated sire breeding values for functional longevity as the number of uncensored progeny per sire increase. This was not unexpected since uncensored records are considered complete and indicate the animal's survival potential. As the number of such daughters increase per sire, its estimated breeding value therefore approaches the true breeding value unlike when censored, incomplete, records are used. In the current study reliability of sires with at least 130 daughters increased reliability of estimates to more than 80%. The objective of any analysis would therefore be to reduce the number of censored animals as much as possible. From the results here-in, reasonable genetic improvement in the length of the productive life can be achieved through selection.

4.6 Conclusion

Heritability estimates obtained with the piecewise Weibull model were higher than those obtained in earlier studies in South African herds with linear, random and threshold regression models. The relatively higher heritability estimates imply that some improvement in the length of productive life, though slow, can be achieved through selection. The genetic evaluation of South African Holsteins should consider inclusion of this trait in the Holstein Profit Ranking Index. The declining average breeding values further reinforce arguments previously presented supporting an attention to functional longevity in South African Holsteins as a way of increasing profitability in dairy herds. The main objective is to ensure that all cows can sustainably achieve the age-dependent maximum yield of milk in herds for longer periods.

4.7 References

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CHAPTER 5

The relationship between conformation traits and functional longevity in South African Holstein cattle

5.1 Abstract

Linear type traits have been used as indicator traits for longevity in dairy cattle based on the medium to high genetic correlation between the traits and longevity measures. A proportional hazards model with a piecewise Weibull baseline hazard was used to determine the contribution of individual body, rump, udder, feet and leg traits on risk of culling among dairy cows. Data from the Holstein Society of South Africa comprising of records from 25 093 cows with 13 type traits measured on a scale of 1 to 9 was used. Analysis used Survival Kit Version 6. Functional longevity was defined as the number of days from first calving to culling or censoring, adjusted for production. Scores (1 to 9) for each type trait and whether an animal had a score or not (1 or 0) were added to the reference model one trait at a time. The reference model included the random herd-year, fixed time-independent effects of age at first calving, time dependent effects of region by year of calving, milk yield production class by year-season, protein and fat percent production classes by year-season, herd size by annual herd size change, the combined number of lactation by stage of lactation by milk yield class. All udder traits evaluated significantly influenced relative risk of culling (P>0.05). Rear teat placement had the largest contribution to the risk of culling. Udder depth, fore udder attachment and median suspensory ligament showed elevated culling risk for very poor scores (score=1). Foot angle contributed to the relative risk of cow culling but rear legs side view (P>0.05) did not. Cows with extremely low foot angle were at the highest risk of being culled (P=0.029). Cows with very low scores for rump height were at a higher risk of being culled from the herds than those with high scores implying a preference for cows superior for relatively ease of calving since . Cows with low scores for chest width were at the highest risk of being culled just as were those with high scores for angularity. Rump width and rump angle did not have a significant influence on the risk of cow culling. Udder traits were the most important traits influencing longevity in South African Holstein cattle. There is potential for selecting animals for longevity on udder type trait information.

Keywords: type traits, survival analysis, conformation, risk of culling

5.2 Introduction

Improving functional longevity in dairy cattle has several advantages all of which contribute to a reduction in production cost in the short to medium term. With increased longevity, the age structure of cows within the herd will shift towards more mature cows with higher production.

The opportunity for voluntary culling i.e. deliberate culling due to low production, increases leading to a reduction in costs associated with involuntary culling, forced culling due to injury, illness, fertility, etc. This implies that the overall cost of cow replacements is paid back over longer time periods of time as functional longevity improves (Berry *et al*., 2005). Opportunities for intensive selection among dams also increase with improved longevity leading to long term increase in production and financial returns to the dairy enterprise. Evidently, the benefits from improved functional longevity outweigh the opportunity cost of selling cull cows and breeding replacement heifers. This makes the trait a desirable candidate for direct selection and improvement. However, rapid genetic progress in the trait is limited by its low heritability which has been reported to range between 0.04 and 0.22 (Ducrocq, 1997; Chirinos *et al*., 2007; Holtsmark *et al*., 2009; Terawaki & Ducrocq, 2009). Besides the low heritability estimate for the trait, a significant amount of records is necessary in order to get reasonable estimates of the genetic parameters and breeding values for sires for longevity. These take a lot of time to gather. This is a limitation in that animals need to be evaluated early in their productive life to avoid keeping an animal that would otherwise be culled for poor longevity and production. There may be need to look at other traits that can be evaluated early in the life of an animal and appropriately used as indicators of functional longevity.

Composite conformation and udder type traits have traditionally been used as indicator traits for herd life and longevity measures (VanRaden & Wiggans, 1995; Weigel *et al*., 1998). This has its advantages. Measured earlier in life, mostly in the first lactation, cows with predicted poor functional longevity as indicated by defective type and conformation traits can be removed from herds earlier without waiting for a large percentage of their female progeny to be culled (Weigel *et al*., 1998). This saves on rearing costs for animals that would otherwise be culled later in life. Furthermore, heritability estimates for some type traits have been reported to be higher (Zavadilová & Štípková, 2012) than for directly measured functional longevity. This implies more relative efficient selection on them than directly on longevity which has low heritability estimates. The relationship between type traits and longevity has been studied since the 1980s (e.g. Jairath & Dekkers, 1994; Boettcher *et al*., 1997; Schneider *et al*., 1999). Procedures were even developed for predicting transmitting abilities for herd life on the basis of the conformation of their daughters using 18 type traits with reliability of up to 0.56 (Boldman *et al*., 1992) although this was criticised by Visscher *et al*. (1994) for being an overestimation of the reliability. The use of type traits as indicator traits for functional longevity was based on the positive and generally low to intermediate genetic correlation between some of them and functional longevity (Bünger & Swalve, 1999; Jovanovac & Raguz, 2011).

South Africa has adopted the measurement and recording of body, udder, stature, feet and leg traits as a method of assisting the dairy farmer in making management decisions. Currently, South African Holstein cattle are evaluated for type traits relating to body, udder, feet and legs as well as stature. These are scored on a scale of 1 – 9 with extremely poor traits scored 1 and the other extreme scored 9. Because of their importance, herds are routinely assessed for type traits, a situation which has increased availability of type traits information that can be used for breeding evaluations and sire selection including for longevity. Previous studies in South Africa have estimated genetic correlation between type traits and longevity as part of a strategy for selecting animals on the latter based on information about the former. Setati *et al*. (2004) reported genetic correlation of 0.41 and 0.48 between longevity and fore udder attachment and fore teat length in the South African Holsteins respectively with a linear bivariate model. Low to medium genetic correlation between longevity and type traits ranging from -0.01 (Thurl width) to 0.35 (Foot angle) were reported for South African Jersey cattle with bivariate linear models (du Toit (2011). Genetic correlations for udder traits were low to medium ranging between -0.03 (Rear tat placement) and 0.49 (udder depth). Elsewhere, Short & Lawlor (1992) found genetic correlations of 0.23 – 0.38 between longevity and udder depth as well as 0.46 – 0.49 for dairy form. These figures were below unity implying that the type traits cannot be considered to be perfect indicators of longevity. The contribution of each of these type traits to the risk of culling would provide better information on the impact of the traits to functional longevity.

Evaluation with survival analysis report significant influence of a number of type traits on longevity (Berry *et al*., 2005; Sewalem *et al*., 2005; Jovanovic & Raguz, 2011; Morek-Kopec & Zarnecki, 2012). Cows with poor final score were observed to be more at risk of being culled than those with a good score. The aim of this study was to estimate the contribution of udder traits, feet and leg traits, rump traits and body traits on the overall risk of culling in South African Holstein cattle using survival analysis methodologies.

5.3 Materials and methods

5.3.1 Data and edits

Production records used in this study were extracted from the INTERGIS of the National Milk Recording Scheme and the conformation data were obtained from the Holstein Society of South Africa. The latter comprised of records of 25 093 cows that calved between 1995 and 2013 with 16 type traits scored on a linear 9-point scale from primiparous cows that were evaluated by trained classifiers. The list of the conformation traits is shown in Table 5.1. Production records were as previously described in sections 3.2 and 4.2. Functional longevity, defined as the ability to resist involuntary culling, was described as the number of days from

first calving to culling or censoring. Data edits were as described in sections 3.2.1 and 4.2.1. Animals without type scores were also included in the analysis as proposed by Larroque & Ducrocq (2001) and were coded 0. Because the proportion of animals with type traits data was low, traits were also evaluated on the basis of whether the animals had a type score (code=1) or not (code=0).

5.3.3 The model

Data were analysed using survival analysis methodology with Survival Kit Version 6 (Ducrocq *et al*., 2010). The model used can be generalised as described in section 4.2 and expressed as: -

$$\lambda(t)=\lambda_{0,ls}(t)\exp\{hy_k(t) + \Sigma_m f_m(t) + tt_i + tp_j\}$$

where $\lambda(t)$ was the hazard function of daughter ***k*** of sire ***s*** with recorded herd life of ***t*** days and hy_k was the random herd-year effect which was assumed to be independently distributed following a log-gamma distribution with both the shape and scale parameters equated to γ so as to force the mean to be 1. In the model, t is the time in days from first calving to culling or censoring. The random herd-year effect was algebraically integrated out and the γ parameter jointly estimated with other effects. $\Sigma_m f_m(t)$ was the sum of all fixed effects as described in Table 3.6 but including each of the 16 type traits. The type traits were each included in the model one at a time.

Table 5.1 Descriptions of linear type traits, their abbreviations (in parenthesis), extreme scores, means and SD

Composite	Trait	Extreme scores		Mean	SD
		1	9		
Capacity	Body depth (BD)	Extremely shallow	Extremely deep	6.42	0.86
	Angularity (ANG)	Coarse	Frail	6.52	0.85
	Chest width (CW)	Extremely narrow	Extremely wide	5.29	1.18
Rump	Rump angle (RA)	Extremely high pins	Extremely low pins	4.81	1.21
	Rump height (RH)	Extremely short	Extremely tall	6.06	1.02
	Rump width (RW)	Extremely narrow	Extremely wide	6.09	0.96
Feet & legs	Rear leg side view (RLS)	Extremely straight	Extremely sickled	5.54	0.83
	Foot angle (FA);	Extremely low	Extremely steep	5.89	1.00
Udder	Fore udder attachment (FUA)	Loosely attached (weak)	Strongly attached	6.10	1.08
	Rear udder height (RUH)	Extremely low	Extremely high	6.23	0.91
	Udder depth (UD)	Extremely shallow	Extremely deep	5.97	1.18
	Udder width (UW)	Extremely narrow	Extremely wide	5.64	1.01
	Median ligament (ML)	Extremely weak	Extremely strong	6.36	1.00
	Fore teat placement (FTP)	Extremely outside	Extremely inside	4.47	0.95
	Front teat length (FTL)	Extremely short	Extremely tall	4.78	1.17
	Rear teat placement (RTP)	Extremely wide	Extremely inside	6.83	1.28

The relationship between function al longevity and type traits were expressed as the relative risk of culling, defined as the ratio of the estimated risk of being culled under the influence of a particular environmental effect relative to the reference class which was set to 1 (Zavadilova *et al*., 2011). The influence of each conformation trait on functional longevity was evaluated with the likelihood ratio tests. These compared the full model with a particular type trait against a reduced model without the trait as previously done by other researchers (Buenger *et al*., 2001; Larroque & Ducrocq, 2003; Sewalem *et al*., 2005). In Survival kit Version 6, this was performed with the TEST LAST procedure of Survival Kit on the fixed effects model (removing the random effects) since this requires less computing capacity than the TEST SEQUENTIAL procedure.

5.4 Results

5.4.1 Effect of absence of type scores

Some cows did not have type scores for a number of reasons. They could have exited herds before they were type scored, the herd might not have been measuring type traits for management purposes or records for the animals were for the period long before national type scoring had commenced. Excluding such animals with missing score causes bias leading to a decrease in the risk of culling (Larroque & Ducrocq, 2001; Morek-Kopec & Zarnecki, 2012). Cows without type scores were more likely to be culled than those with type scores. Figure 5.1 shows the relative risk of culling for animals with type scores against the reference class, animals without type scores. Animals with type scores were 0.81 to 0.94 times less likely to be culled than those without scores. The narrow difference in risk ratios for animals without type scores and those with scores for all traits may point to the fact that farmers were not completely utilizing type information for culling.

5.4.1 Effects of type traits on functional longevity

Of the 17 recorded type traits, only 11 were included in the analysis. These comprised of five udder traits (Fore udder attachment, udder depth, udder width, rear teat placement and median suspensory ligament), three rump traits (rump angle, height and rump width), two traits related to feet and legs (foot angle and Rear leg side view) as well as one body trait (chest width). The excluded traits had less than 50 uncesnored records for some of the classes thereby compromisisng accuracy of estimation of relative risk ratios. Table 5.2 shows the results of the statistical significance tests of type traits on functional longevity. The overall contribution of the evaluated traits to functional survival was very small, at less than 5%. This was probably because the data set used in this analysis had a lot of animals that were in the first lactation well before

type scoring was holistically adopted among the herds on the milk recording scheme. However, all measured udder traits had a significant effect (P<0.05) on the relative risk of culling. Cows with extremely low foot angle were at a significantly higher risk (P<0.05) of being culled than those with extremely steep foot angles. However, legs rear side view did not influence (P>0.05) the ability of the animals to resist culling. Longevity was also influenced by all the included rump traits, chest width and angularity (P<0.05). Traits with the biggest change in the log likelihood, rear treat placement, udder depth, angularity, median suspensory ligament and fore udder attachment had relatively the greatest influence on the cows' probability of being culled.

5.4.1 Effect of individual linear systems

5.4.1.1 Udder traits

Udder type traits, when measured early in productive life of a cow, are important for the prediction of the cow's milk producing ability. Recently, they have also become an important determinant of the functional longevity of the animals due to their influence on udder health and milkability. Animals with scores for udder traits were 0.81 to 0.94 times less likely to be culled than those without a type score for any of the udder type traits. All udder traits included in analysis had a significant effect (P<0.0001) on cow longevity.

Rear teat placement contributed the most to the risk of cow culling followed by rear udder height, udder depth, fore udder attachment and median suspensory ligament in that order. Cows with extremely deep udders, close to the ground, were 2.35 times more likely to be culled than the average cows (class 5) whilst those with very shallow udders (class 9) were 0.929 times less likely to be culled than the average cows. Udder traits related to suspension of the udder, median ligament and fore udder attachment, showed a significant influence on the risk of culling. Animals with weak fore udder attachment were more than 1.24 times more likely to be culled than the average cows whilst those with strong attachments were 0.949 times less likely to be culled than the average cow. Extremely weak median ligament predisposed cows to culling although cows without scores for median ligament were 83% (RR=1.946) more likely to be culled that the average cows. Good scores for median ligament led to low risk of culling among the cows (RR=0.875). Cows with weak fore udder attachments were probably culled because the loosely attached udders are associated with pendulous udders that predispose animals to high incidence of mastitis and mobility problems. The condition of the median suspensory ligament was almost linearly related to the relative risk of culling of cows. Fore teat placement and fore teat length

were excluded from the analysis because there had less than 50 uncensored records for some of the classes which would compromise accuracy of estimation of relative risk ratios.

Table 5.2 The change in -2 log likelihood for linear traits (-2LL=1 411 876.09; 25 093 cows and DF=9)

Trait	DF	-2LL including type trait	-2ΔLL	P-value	R^2 for MADDALA
Fore udder attachment	9	1 411 673.835	202.26	P<0.0001	0.2139
Udder depth	9	1 411 648.958	227.13	P<0.0001	0.2139
Udder width	9	1411 696.015	180.07	P<0.0001	0.2139
Rear teat placement	9	1 411 568.173	307.92	P<0.0001	0.2139
Median ligament	9	1 411 674.074	202.02	P<0.0001	0.2139
*Rear leg side view (leg set)	9	1 411 700.390	175.69	P>0.05	0.2139
Foot angle	9	1 411 690.907	185.19	P<0.0001	0.2139
Chest width	9	1 411 687.883	188.20	P<0.0001	0.2139
Rump angle	9	1 411 695.592	180.49	P<0.0001	0.2139
Rump height	9	1 411 695.650	180.44	P<0.0001	0.2148
Rump width	9	1 411 700.748	175.34	P<0.0001	0.2139

*Non-significant (P>0.05)

Cows with extremely outside rear teat placements were more than 4.5 times more likely to be culled than the average cows. Cows with rear teats that were extremely inside were 0.99 times less likely to be culled than the average cow. The relationship between rear teat placement and risk of culling was not linear indicating farmers tended to cull cows on this trait if and only if the score was very poor. Cows with scores of 2 to 8 were retained in the herds with almost identical though declining relative risk. Cows with medium scores (3 to 7) had a marginal predisposition to resist culling for poor type. Fore teat length and fore teat placement demonstrated an intermediate optimum. For fore teat length, animals were generally culled for very short teats and very long teats with those cows within intermediate scores (4 to 7) being able to marginally resists culling. Similarly animals with extremely outward or extremely inward placed teats were most likely to be culled whilst those with intermediate scores, 4 to 8, being able to resist involuntary culling.

5.4.1.2 Feet and legs

Feet and legs are important as they indicate the ability of the animals to sustain the extra weight of pregnancy as well as mobility within pasture for feeding. The latter is achieved through

prediction of the cow's ability to resist lameness. Cows with type scores for foot and leg traits were, on average, 0.88 to 0.92 times less likely to be culled than those without type score. Foot angle had a significant effect on the risk of culling (P=0.029) whilst the effect of rear leg set was not significant (P=0.4286). Although non-significant, rear leg set demonstrated an intermediate optimum with low relative risk of culling for cows with scores between four and seven. Cows with extremely straight rear legs were 1.966 times more likely to be culled than the average cows just as those with extremely sickled legs were more likely to be culled than the average cows (RR=0.966). Rear leg conformation is also important as it determines the ease and efficiency of the milking process. Usually, cows with extremely toe-out legs are highly predisposed to culling just as are those with extreme toed-in legs. The former usually have large udders, are high yielding and easily expose the udders for teat cup insertion during milking. Farmers will tend to keep such animals despite the risk of leg and udder injury the latter leading to possible mastitis. The relative risk values for feet and leg traits are shown in Table 5.3.

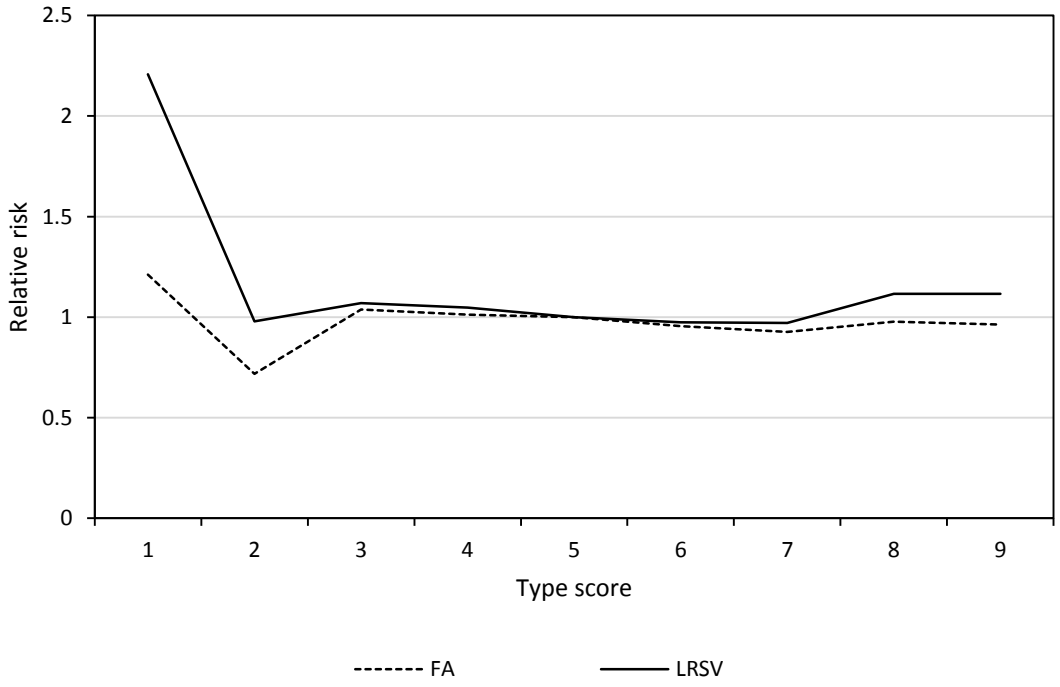

Figure 5.1 Relative risk estimates for foot angle (dotted line) and leg rear side view (solid line)

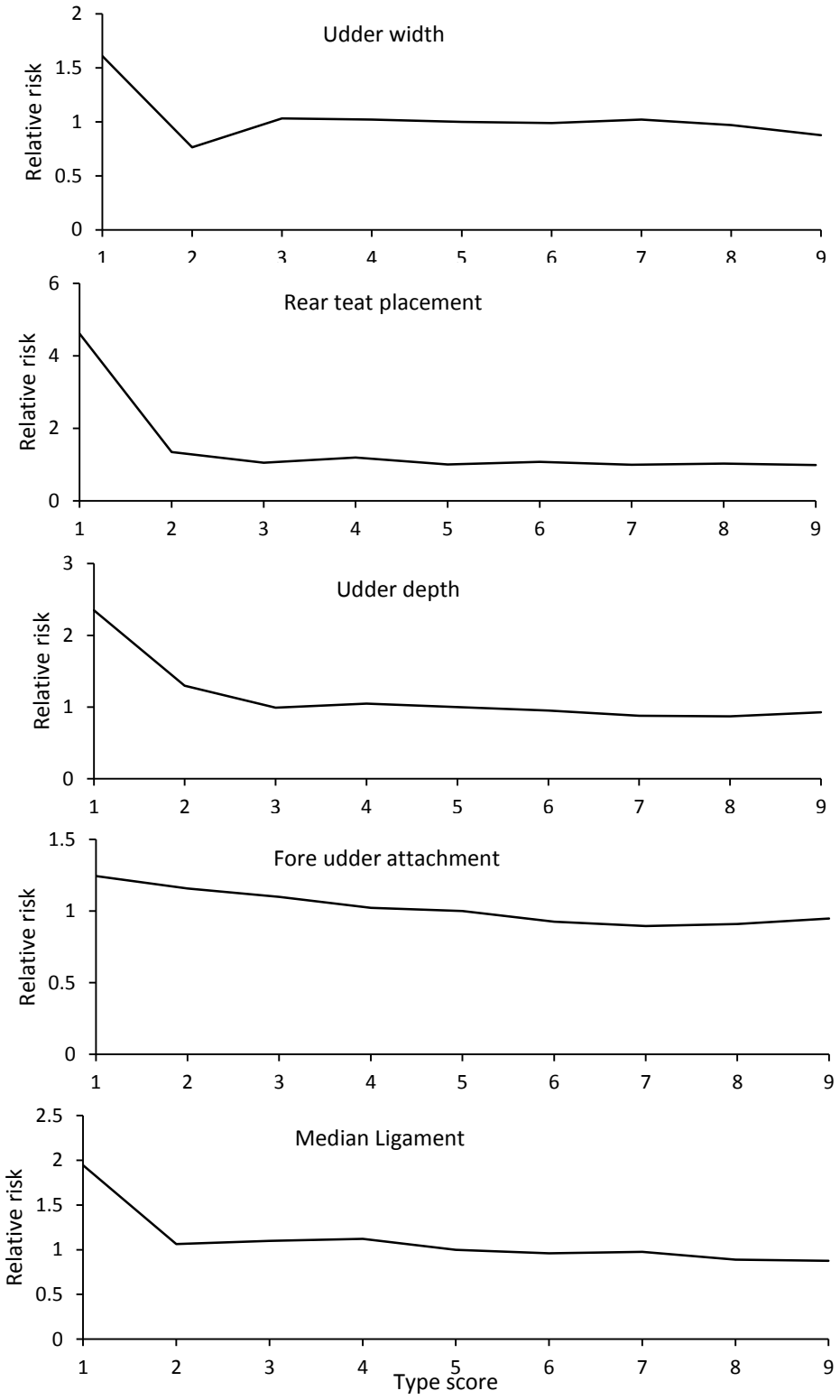

Figure 5.2 Relative risk estimates for udder depth, udder width, rear teat placement (RTP), fore udder attachment and median ligament

5.4.1.3 Body traits and rump traits

Body traits are directly related to the amount of feed an animal can take in and its respiratory system. Both are indicators of the efficiency of metabolism that is critical for milk production and maintenance. They also indicate the internal ability of the animal to sustain the developing foetus during pregnancy. Values for relative risk of culling of cows on body and rump traits are in Table 5.3. Cows with type scores for body traits were 0.89 to 1.003 times likely to be culled than those without a type score. Cows with extremely narrow chest width were highly predisposed to culling (RR=3.346) whilst cows with very shallow body depth and very coarse angularity had very low risk of being culled.

Rump traits are related more to stature and indirectly with calving ease, a known issue in dairy cattle reproduction. Cows with extremely narrow rumps (RR=1.312), extremely short rump height (RR=2.817) and extremely high rump angle (1.061) had relatively higher risk of being culled than the average cows for the respective type scores. Within the score range of 3 to 9, there was very little influence of rump type traits on culling although marginal increases were observed at the higher end (score=9) for rump height (RR=1.191). All body and rump traits had a significant influence on longevity (P<0.0001). Body depth and angularity were not included in the analysis because of low numbers of uncensored daughters for sires for the traits.

Table 5.3 Relative culling rates for of cows for feet and leg, body and rump traits (relative risk of class 5 set to 1)

Score	Body and rump traits				Feet & Legs	
	RA	RH	RW	CW	LRS	FA
1	1.061	2.817	1.312	3.346	1.966	1.516
2	1.120	1.006	0.704	1.104	0.931	0.682
3	1.000	1.001	1.002	0.989	1.051	1.019
4	1.037	0.989	1.011	0.958	1.049	1.008
5	1.000	1.000	1.000	1.000	1.000	1.000
6	1.011	0.971	1.009	1.028	0.992	0.977
7	1.047	0.962	1.021	0.950	0.995	0.953
8	0.921	1.050	1.029	0.970	1.153	0.977
9	0.912	1.191	0.565	0.874	0.996	1.015

5.5 Discussion

As in previous research (e.g. Buenger *et al*. 2001), this study evaluated the influence of type traits on longevity thereby assisting in identifying those type traits important for the total functionality of the cow and longevity. Udder traits had a greater influence on functional longevity than rump, body, feet and leg traits. Cows without type scores were at higher risk of being culled than those with scores (RR=0.81 to 0.94) for all traits. This was consistent with results obtained for Polish Holstein cattle (Morek-Kopec & Zarnecki, 2012).

5.5.1 Udder traits

Udder traits are closely associated with dairy form and are also very important pointers of udder health and cow's milkability. Udder traits contributed the most to the risk of culling in South African Holsteins. Similar results were observed among German Holstein-Friesian cattle (Buenger *et al*., 2001), New Zealand Holstein-Friesian and Jersey cattle (Berry *et al*., 2005) US Holsteins (Caraviello *et al*., 2004), Czech Holsteins (Zavadilova *et al*., 2011), Canadian dairy cattle (Sewalem *et al*. 2004 &2005) and Polish Holstein-Friesian (Morek-Kopec & Zarnecki, 2012). Analysis showed a positive relationship between functional longevity, as indicated by risk of culling, and all the evaluated udder traits. Fore udder attachment showed an almost linear. Trends for other udder traits showed greater risk of culling for cows with extremely low scores than higher scores. Among the udder traits, median ligament, fore udder attachment and udder depth were significantly associated with functional longevity. These are all associated with udder support which is critical for maintenance of udder health. In French Holsteins, Larroque and Ducrocq (2001) reported the highest contribution to risk of culling for median ligament and udder depth. Schneider *et al*. (2003) and Sewalem *et al*. (2004) reported highest risk of culling for rear udder attachment, fore udder attachment, udder depth and median ligament. In Czech Holstein cattle, Zavadilova *et al*. (2011) reported udder depth, fore udder attachment and median ligament as the traits with greatest influence on risk of culling and therefore finctional longevity. Cows with poor udder support develop pendulous udders that predispose the mammary organ to injuries which might lead to mastitis. Mastitis management is costly for the dairy enterprise.

Rear teat placement contributed the most to the risk of culling. Animals with extremely wide rear teats were at a greater disposition to be culled. These extremely toed-out rear teats are undesirable since they interfere with the cow's mobility. They also interfere with the efficiency of the milking process. Extremely toed-in rear teats may not be desirable as well because they also interfere with teat cup placement during milking. Cows with extremely toed-in fore teats were at

higher risk of being culled than those with extremely toe-out fore teats. This was contrary to trends reported by Buenger *et al*. (2001), Larroque & Ducrocq (2001) and Sewalem *et al*. (2004).

5.5.2 Feet and leg traits

The contribution of feet and leg traits to the risk of culling was low as was also observed among New Zealand Holstein-Friesian cattle (Berry *et al*., 2005), Polish Holstein Friesian cattle (Morek-Kopec & Zarnecki, 2012), Czech Holsteins (Zavadilova *et al*., 2011), French Holsteins (Larroque & Ducrocq, 2001). Foot angle had an almost linear and significant influence (P=0.029) on the culling risk as previously reported elsewhere (Caraviello *et al*., 2004; Schneider *et al*., 2003). Cows with low foot angles were at higher risk of being culled than the reference class animals. The effect of rear leg side view on functional longevity was small and non-significant although the result indicated that animals with extremely straight legs were at higher risk of being culled than those with sickled legs. There has been a lot of inconsistencies in the relationship between functional longevity and feet and legs traits. Contrary to results herein, Zavadilova *et al*. (2011) and Dadpasand *et al*. (2008) reported minimal effect of foot angle on longevity although they acknowledged, as in this study, that the trait contributed to the risk of culling. Earlier studies (Buenger *et al*., 2001) reported significantly greater contribution of foot angle to the risk of culling than rear leg set whilst Sewalem *et al*. (2005) reported a significant effect of rear leg side view on functional longevity and that the trait contributed more to the risk of culling than foot angle but it showed an intermediate optimum. Buenger *et al*. (2001) and Sewalem *et al*., (2004) reported an intermediate optimum for rear leg side view implying that only those cows that had type scores within the intermediate range where retained. Cows with extreme scores had a high predisposition to be culled.

5.5.3 Body and rump traits

The contribution of body and rump traits to the risk of culling was low but significant (P<0.0001). The former assist in determining the ability of the cow to sustain high production as per her genetic potential without loss in condition which might compromise her productivity. Chest width of South African Holstein cattle significantly influenced longevity. The risk of culling was high for cows with extremely narrow chests and low for those with wide chests. This concurred with results from Sewalem *et al*. (2004) and Schneider *et al*. (2003) who reported high risk of culling for cows with narrow chest and low risk of culling for cows with wider chest (score=9). By implication, farmers were inclined to cull cows with narrow chest as they are perceived to have dimished respiratory capacity. This is directly associated with efficiency of metabolism necessary for milk production

and maintenance. By contrast, Morek-Kopec & Zarnecki (2012) reported an intermediate optimum peaking at score of two for chest with in Polish Holstein-Friesian and the risk of culling increased with score for the trait.

Rump height was mildly intermediate optimum. Cows with extremely high pins and those with narrow rump angles had a lower chance of surviving than those with lower pins and wider rumps respectively. Farmers prefered cows with intermediate rump angle. Poor rump scores are indicative of possible calving difficulties especially in young cows. Berry *et al*. (2005) reported a low influence of rump related traits on functional longevity whilst Schneider *et al*. (2003) observed a large contribution of the rump composite traits to the overall risk of culling. These observed differences in trend can be attributed to differences in trait definition (Berry *et al*., 2005).

5.6 Conclusion

The piecewise Weibull model provided a better description of the relationship between functional longevity and type scores than previously used linear models. All type traits analysed in this study had a significant influence on functional longevity except rear leg side view. For all the traits, risk of culling is elevated for the extreme undesirable type score of one and significantly reduced for all the other scores among South African Holsteins. Udder traits have the greatest influence on the risk of culling with rear teat placement contributing the most to the probability of cows being culled. High type scores for traits associated with udder support: udder depth, median suspensory ligament, fore udder attachment and rear udder height are desirable for increased longevity within herds. The risk of cow culling on the basis of fore teat length and fore teat placement demonstrated an intermediate optima favouring intermediate scores of 4 to 7. Body and rump traits have significant but low contribution to risk of culling. Udder traits, foot angle, chest width and rump traits can all be used as indicators of functional longevity in South African Holstein.

5.7 References

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6 General conclusions and recommendations

Based on the genetic parameter estimates of obtained from this study, the adoption of survival analysis methodology for routine genetic evaluation of South African Holsteins for functional longevity is justified. The methodology better accounts for time-dependence of covariates, non-normal distribution of survival data and better handle censored records. Suvival models enhance the accuracy of prediction (reliability) of breeding values. As demonstrated through the plots of the empirical hazard function for the first three lactations of cows and the trends in the value of the Weibull shape parameter, use of a piecewise Weibull model is also justified.

Phenotypic and genetic measures of functional longevity in South African Holsteins showed a decreasing trend. This could be attributed to absence of genetic selection among Holstein sires for functional longevity in South Africa. The decline in genetic trends could be due to intense selection for production traits. Intensive selection for production is known to reduce genetic progress for functional longevity.

Milk production is the major deteminant of the decision to cull Holstein cows in all the six regions of South Africa. High yielding cows are kept for longer periods in herds than low yielders. Cows in the Northern Cape, Western Cape and Kwa Zulu Natal had the best longevity when compared with those in the Eastern Cape, the Free State and combined Gauteng/North Western provinces specifically for cows that calved for the first time in 2002. Functional longevity was also influenced by the combined effect of annual herd size change. Cows in shrinking and stable herds were more predisposed to culling than those in expanding herds. Heifers calving at a younger age, 22 months, had better functional longevity than those calving at an older age and those calving at very age. Heifers calving at an old age could be indicative of fertility problems. On the other hand, heifers calving for the first time at a very young age, below 22 months of age, had higher relative risk of culling than the average animals probably because of calving difficulties common in young heifer. Relative risk of culling was lowest during the first stage of lactation for all lactations and it was highest during the second stage of lactation for all lactations probably because farmers tend to remove from herds cows that fail to return to cycling after calving as well as poor yielders. Relative risk declines in second stage of lactation probably due to the combined effects of old age and stage of lactation

Heritability estimates for functional longevity in this study were found to be about 11%. These were higher than previous estimates obtained on South African Holsteins with linear models. There are prospects for genetically improving longevity through breeding and selection although the process could be slow because of the magnitude of the heritability. The accuracy of estimation of the genetic parameters depends on the number of uncensored daughters of the sires. The higher the number of uncensored, complete records, the more accurate the estimation of parameters. This would again require a considerable number of completed records. Selection for functional longevity on type traits still provides a viable strategy for early selection for longevity. All type traits evaluated in this study significantly influenced functional longevity except leg rear side view. These can therefore be used as indicator traits for longevity. Besides, they have been reported to have higher estimates of heritability that longevity implying more rapid progress than the latter.

From the results of this study, it is hereby recommended that: -

Milk recording be customised to allow collection of data that can be evaluated appropriately with survival analysis techniques.

i Milk recording should emphasize on the need to appropriately capture all herd events particularly those involving cow exits and entries into herds through death, culling for specified health issues, type traits or sales or any other entry/exit method.

ii All animals on milk recording scheme be scored for udder, body, rump, feet and leg traits and availability of the data coordinated with the production data for efficient genetic evaluation of animals.

iii Sires be routinely evaluated for functional longevity as is done with production traits and functional longevity incorporated into the Holstein Ranking Index for South African cattle.

Iv A piecewise Weibull proportional hazards model be adopted for estimation of sire breeding values for functional longevity in South African Holstein cattle.

7. APPENDICES

7.1 Lactation records obtained from INTERGIS

LACTATION RECORDS	
Animal (cow) identity;	Lactation number;
Dam identity;	Herd status (registered or commercial)
Sire identity;	Actual milk yield;
Herd code;	Adjusted 305-lactation yield;
Date of cow (animal) birth;	Protein yield;
Date of calving;	BFC yield;
Last date of lactation (lactation end date);	Termination codes; and
Date of death of cow;	Region

7.2 Type and conformation records

Type and conformation records
Body depth (BD);
Angularity (ANG);
Chest width (CW);
Rump angle (RA);
Rump height (RH);
Rump width (RW);
Rear leg set (RLS);
Rear leg rear view (RLRV);
Foot angle (FA);
Fore udder attachment (FUA);
Rear udder height (RUH);
Rear teat placement (RTP);
Fore teat placement (FTP);
Fore teat length (FTP);
Udder depth;
Udder width;
Central/Median ligament.

7.3 Termination codes

Code	Termination freason
01	Normal lactation
03	Sold for dairy reasons
04	Died
05	Aborted (>210 days since last calving date)
06	Brucellosis (Contagious abortion)
07	Tuberculosis
08	Low production
09	Herd withdrawn
13	Culled – Low production
14	Infertility
15	Conformation – udder
16	Conformation – feet and legs
17	Mastitis
18	Injury
19	Clinical (health) reasons
20	Not tested this lactation (i.e no test records)